GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd. 3.5

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Database
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Maximum Match 100%
Listing first 45 summaries
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A Geneseq 19Jun03:*

1: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1107863 seqs, 158726573 residues
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1 MKLTTDYPLLKNIHTPADIR.....LSLVGLDSKGILATIEQFCA 620
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match Length DB	ength	BB	ID	Description
۲,	3216	-	620	23	ABG61581	High growth methan
N	3216	100.0	620	23	AAE22301	Methylomonas 16a s
w	3216	100.0	620	23	AAU80325	Methylomonas 16a O
4	2069.5	64.4	627	22	AAU00012	Pseudomonas aerugi
ű	2069.5	64.4	627	23	AA021846	Isoprenoid related
თ	2063.5	64.2	627	22	AAU00014	Pseudomonas aerugi
7	2061.5	64.1	627	22	AAU00013	Pseudomonas aerugi
80	2014.5	62.6	620	22	AAU38490	Salmonella typhi c
9	2000.5	62.2	620	20	AAY52832	Escherichia coli p

Koffas M, Odom JM, WPI; 2002-452200/48.

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Schenzle A;

bidopsis	AAG42535	21	632	43.2	1389.5	ű
. piperita	AAY14144	20	721	43.3	1392	4
Isoprenoid related	AA021848	23	633	43.4	ω	ü
tili	AAB20543	21	633	43.4	1394.5	2
Symechocystis sp.	AAB20542	21	633	•	w	Ξ
Isoprenoid related	AA021849	23	735	•	1402	ö
oprenoid relate	AA021851	23	719	•	1402.5	9
thaliana DOXS	166	21	717	•	1404.5	8
DOXS	AAY51612	2	717	•	1404.5	37
cter	AAY52833	20	637	•	1406.5	6
ecta p	AAY15157	21	725		1407.5	ű
Soybean 1-deoxy-D-	AAY97414	21	721	•	1410.5	4
Isoprenoid related	AA021854	23	641	•	1410.5	ü
Thioredoxin/deoxyx	AAM48247	23	824		1411.5	ö
Arabidopsis thalia	AAM48245	23	717	•	1411.5	μ
Arabidopsis thalia	AAG42534	21	717	•	1411.5	ö
Truncated deoxyxyl	AAM48246	23	659	•	1411.5	29
Isoprenoid related	AA021855	23	637	٠	1411.5	8
piperita	AAY14146	20	727	•	1418.5	27
ب	AAY14145	20	724	•	1418.5	95
Soybean 1-deoxy-D-	AAY97415	21	708		1420.5	25
Isoprenoid related	AA021857	23	636	•	1439	4
Isoprenoid related	AA021858	23	640	٠	1442	23
Rice 1-deoxy-D-xyl	AAY97422	Ŋ	720		4	22
Isoprenoid related	AA021856	23	648	•	1491.5	21
Rhodobacter sphaer	AAY52834	20	648		504.	ö
soprenoid	AA021845	23	641		532.	13
prenoid rela	AA021847	23	628		6	8
. gonorrho	ABP77532	24	637		1774	7
relate	AA021861	23	637	•	1776	16
soprenoid	AA021862	23	625		1937.5	15
soprenoid	AAO21860	23	620		2000.5	14
. coli cellular	AAU34475	22	620		2000.5	3
. coli DOXS prot	AAY51613	21	620		2000.5	12
cherichia coli	2054	21	620	62.2	2000.5	11
. coli DXS	AAY08880	20	620		2000.5	0

ALIGNMENTS

ğ	PR	ž	ΡF	ğ	Gd	ğ	PN	X	g	ğ	Œ	Ÿ	걸	Ş	즟	¥	Ħ	B	Ħ	DI	ğ	Ã	ğ	ij	RESULT 1 ABG61581
	01-SEP-2000; 2000US-229858P.		28-AUG-2001; 2001WO-US26827.		14-MAR-2002.		WO200220728-A2.		Methylomonas 16a.		nitrous oxide; terpenoid; animal feed; carotenoid; exopolysaccharide.	methane-containing environment; waste water treatment system; isoprenoid;	ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill;	pyrophosphate dependent phosphofrutokinase; nitrogen-containing compound;	methane; methanol; Embden-Meyerhof carbon flux pathway; 16s RNA;	High growth methanotrophic bacterial strain; C1 carbon substrate; enzyme;		High growth methanotrophic bacterial strain polypeptide #31.		27-AUG-2002 (first entry)		ABG61581;		ABG61581 standard; Protein; 620 AA.	57 1 1581

New high growth methanotrophic bacterial strain, useful for producing single cell proteins, grows on a Cl carbon substrate, and comprises a functional gene encoding in Embden-Meyerhof carbon pathway 157pp; English

The invention relates to a high growth methanotrophic bacterial strain, comprises a functional Embden-Meyerhof carbon flux pathway comprising a comprises a functional Embden-Meyerhof carbon flux pathway comprising a comprise a pyrophosphate dependent phosphofrutokinase enzyme or a 16s compression and for the biotransformation of a nitrogen-containing compound, compound, nitrate, nitrite or nitrogen. It is also useful for the production of a feed product comprising a protein, carbohydrates and a compression of a protein, carbohydrates and a compression of a feed product comprising a protein, carbohydrates and a compression of a containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are containing environments such as landfills, waste the present. The bacterial strain of the invention can be used as a containing compound of a protein can be used as a containing environment of the containing environment of nitrate or nitrite to nitrous condex with methane or methanol as a carbon source. It is also used in the containing environment in the containing environment in the protein of the protein o

Sequence 620 AA;

Similarity

100.0%; 100.0%;

Score 3216; DB 23; Pred No 1.2e-285;

Length

620;

8 В Ś Db Ś 맑 Ś 맑 δ 9 Ś 밁 Ś B S 밁 Q 몺 8 Query Match Best Local S Matches 620 421 421 361 361 301 301 241 241 181 181 121 121 620; 61 61 HSSTSISAALCMAIASQLRGEDKKMVAIIGDGSITGGWAYEAMNHAGDVNANLLVILNDN MKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVS1SGGHFAAGLGTVELTV MKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTV ALHYVFNTEVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVG DMSISPPVGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGT HSTSISAALGMA LASQERGEDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILADN ALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREEL PGAAIDPTLTALBIGKAEVRHHGSRIAILAWGSWVTPAVEAGKQLGATVVNMRFVKPFDQ 540 AGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQHHGPASVRYPRGKG NRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDR NRYFDVAIAEQHAVTLAAGQACQGAKÞVVAIYSTELQRGYDQLIHDVALQNLÐMLFALDR PATDTTKDTLFKAAPSPHETYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFP LFBELGENYFGPIDGHDVBMLVSTLENLXDLTGPVFLHVVTKXGXGYAPAEKDPLAYHGV LFEELGFNYFGPIDGHDVEMLVSTLENLXD1TGPVFLHVVTKKGKGXAPAEXDPLAYHGV DWSISPPVGAMNNYLTKVLSSKPYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGT ALHYVFNTEVDQLVMDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVG AGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGPQHHGPASVRYPRGKG PAFDPTKDFLPKAAPSPHPTYTEVPGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFP Conservative 0 Mismatches 0 Indels 0 Gaps 180 60 60 480 420 360 360 300 300 240 180 120 120 540 480 420

> 븅 닭 δ RESULT Carotenoid; isopentenyl pyrophosphate; antheraxanthin; danti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; D-1-deoxyxylulose-5-phosphate synthase; Dxs. AAE22301 standard; Protein; 620 01-SEP-2000; 01-SEP-2000; 07-MAR-2002 Methylomonas 16a Methylomonas 16a sp. D-1-deoxyxylulose-5-phosphate 25-JUL-2002 producing carotenoid compounds e.g. antheraxanthin and astaxanthin, using microorganisms having a mucleic acid molecule encoding enzyme the carotenoid biosynthetic pathway and which metabolize single car 04-SEP-2001; 2001WO-US27420 Claim 41; substrates (BURO 541 2002-351711/38. DU PONT DE NEMOURS & LSLVGLDSKGILATIEQFCA LSLVGLDSKGILATIEQFCA 620 Page 109-111; 156pp; English. Picataggio PC, 2000US-229858P. 2000US-229907P. (first Cheng Q, Iggio SK, ģ entry) Ó Rouviere Dicosimo 8 620 Ħ ,ad Koffas Z synthase (Dxs) 600

encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. D-1-deoxyxylulose-5-phosphate synthase (Dxs) The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the used in the invention

Sequence 620 AA;

8 Ś Query Match Best Local 9 Similarity MKLTTDYPILKNIHTDADIRALSKDQLQOLADEVRGYLTHTVSISGGHFAAGLGTVELTV MKLITTDYPELKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTV 100.0%; Score 3216; DB 23; Pred. No. 1.2e-285; ; Mismatches 0; Length 0; Gaps 60 60

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ALSULT 3
AAU80325
ID AAU8
XX AAU8
AC AAU8
XX Meth
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Schenzle
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                                                                                                                                                                                                                                                                                                             14-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                              Methylomonas sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive; keratenoid; pigment; flavour; fragrance; open reading frame 1; ORF1 dxs; 1-deoxyxylulose-5-phosphate synthase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methylomonas 16a
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DB; ABK50081.
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                                                                           Koffas M,
A, Tomb J;
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Novel nucleic isolated from compounds -
                                                                                                      acid molecule encoding a isoprenoid biosynthetic Methylomonas 16a, useful for the production of is
                                                                                                      ic enzyme, isoprenoid
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Claim 4; Page ; 89-99 84pp; English

an isopremoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an isopremoid compound biosynthetic enzyme, and for the microbial production of isopremoid compounds. The molecules of the invention are also useful for regulating isopremoid biosynthesis in an organism and for producing recombinant organisms for producing various isopremoid compounds. The mucleic acid is also useful for feed additive, for the production of keratemoids and their derivatives, isopremoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 1 (ORF1) dxs (1-deoxyxylulose-5-phosphate synthas enzyme) protein of the invention, as described above. The present invention relates to a new nucleic acid molecule encoding synthase

Sequence 620 AA;

Length

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620; Conserv
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LSLVGLDSKGILATIEQFCA
                                                             ALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREEL
                                                                                              PGAAIDPTITALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNWRFVKPFDQ
                                                                                                                                               AGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFOHHGPASVRYPRGKG
                                                                                                                                                                                             NRYFDVALAEQHAVTLAAGQACQGAKPVVALYSTFLQRGYDQLIHDVALQNLDMLFALDR 420
                                                                                                                                                                                                                                                              PAFDPTKDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFP
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                                                                                                                                                                                                                                                                                                                                                                                                             HSSTSISAALGMALASQLRGEDKKWVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                               ALHYVFNTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTV
                                                                                                                                                                                                                                                                                                LFEELGFNYFGPIDGHDVBMLVSTLENLKDLTGPVFLHVVTKXGXGYAPAEKDPLAYHGV
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                                                                                                                                                                                                                                              PARDPTKOFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEPSQKFP
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                                                ALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREEL
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llarity 100.0%;
Conservative 0
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Pred. No. 1.2e-285;
; Mismatches 0;
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RESULT

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                                                                                                                                                                     CC in meed of enhanced or inhibited activity or expression of or cimmunological response to dxs. Dxs and the nucleic acid encoding it are useful as diagnostic reagents, especially in relation to diseases related CC to expression or activity of dxs. Fragments of the nucleic acid are CC useful as probes or primers and to synthesise full length dxs CC polynucleotides. The nucleic acid and protein are useful for diagnosing bacterial infections, especially by Pseudomonas aeruginosa, staging a CC disease or response of an infectious organism to drugs, and are also used in a structure based design of an (ant)agonist to dxs. The nucleic acid, CC protein and antibodies raised against it are useful for screening for the initial physical interaction between a pathogen and a mammalian host responsible for sequelae of infection. These molecules are useful in CC preventing adhesion of gram positive and/or gram negative bacteria to CC eukaryotic extracellular matrix proteins or in-dwelling devices or in CC opthogenesis in infections initiated other than by the implantation of CC in-dwelling devices or by other surgical techniques. Dxs is also useful CC in-dwelling devices or by other surgical techniques. Dxs is also useful CC are useful for treating Helicobacter pylori infection, and also to CC carefinoma.
                                                                  Matches
                                                                                Query Match
Best Local
                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deoxyxylulose-5-phosphate synthase; dxs; agonist; antagonist; diagnostic; eukaryotic extracellular matrix protein; antibody; wound; in-dwelling device; Helicobacter pylori infection; gastric ulcer; gastrits; gastrointestinal carcinoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 4; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New deoxyxylulose-5-phosphate (dxs) polypeptides of Pseudomonas aeruginosa useful for diagnosis of dxs expression or activity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Huang J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence represents Pseudomonas aeruginosa deoxyxylulose-5-phosphate
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DB; AAS00017.
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                                                                                Similarity
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PLLDRASSPAELRRIGEADLETLÄDELRQYLLYTVGQTGGHFGAGLGVVELTIALHYVFD 75
                        PLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVFN 67
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                                                                                                                                627 AA;
                                                                 Conservative
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                                                               Score 2069.5; DB 2:
Pred. No. 1.7e-180;
0; Mismatches 117;
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Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                                                                WPI;
                                                                                                                                                                    Gokarn
                                                                                                                                                                                                                                                                           29-SEP-2000; 2000US-236580P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pseudomonas aeruginosa
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                                             AAU00014;
                                                                           AAU00014 standard;
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(first entry)

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Query Match Best Local Matches

Similarity

64.28; 100; Score Pred.

Conservative

Mismatches No. 6.16

118; DB 22;

Indels Length

627; 7; Gaps

.1e-180;

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The sequence represents Pseudomonas aeruginosa deoxyxylulose-5-phosphate cynthase, dxs, temperature sensitive mutant, ts-80. (Ant) agonists of dxs care useful for treating an individual in need of enhanced or inhibited activity or expression of or immunological response to dxs. Dxs and the cucleic acid encoding it are useful as diagnostic reagents, especially in certain to diseases related to expression or activity of dxs. Pragments of the nucleic acid are useful as probes or primers and to synthesise control in the serious pacterial infections, especially by Pseudomonas control in the serious or acid and protein are useful for drugs, and are also used in a structure based design of an (ant) agonist to dxs. The nucleic acid, protein and antibodies raised against it are useful for screening for (ant) agonists of dxs or the nucleic acid and are useful in preventing adhesion of prampositive and or pathogen and a mammalian host responsible for sequelae of infection. These molecules are useful in preventing adhesion of gram positive and/or gram negative bacterial to eukaryotic extracellular matrix proteins or confidence or indevices or in wounds; to block bacterial adhesion; to block the normal progression of pathogenesis in infections initiated other than the implantation of in-dwelling devices or by other surgical confidence. Dxs is also useful for identifying membrane bound or soluble receptors. The (ant) agonists are useful for treating Helicobacter pylori infection, and also to prevent, inhibit or treat gastric ulcers, confidence of the dxs sequence given in AAU00012.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New deoxyxylulose-5-phosphate (dxs) polypeptides of Pseudomonas aeruginosa useful for diagnosis of dxs expression or activity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnostic; eukaryotic extracellular matrix protein; antibody; wound; in-dwelling device; Helicobacter pylori infection; gastric ulcer; gastritis; gastrointestinal carcinoma; mutant; mutein; ts-32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page - ; 41pp; English
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RESULT 7
AAU00013
ID AAU0
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XX Deox
XW diag
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XW diag
XW gast
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XX P
   Huang
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                                                                                                                                                                                                                                 16-AUG-2000; 2000WO-US22332.
                                                                                                                                                                                                                                                                                                            01-MAR-2001
                                                                    (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Deoxyxylulose-5-phosphate synthase; dxs; agonist; antagonist; diagnostic; eukaryotic extracellular matrix protein; antibody; wound; in-dwelling device; Helicobacter pylori infection; gastric ulcer; gastritis; gastrointestinal carcinoma; mutant; mutein; ts-32.
                                                                                                                                                                                                                                                                                                                                                                             WC200114409-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Misc-difference
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                                                                SMITHKLINE BEECHAM CORP. SMITHKLINE BEECHAM PLC.
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Jiang X,
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                                                                                                                                                                    9905-0377279.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Wild-type Pro replaced by Ser"
   McDevitt D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ts-32 mutant.
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Sequence

627 AA;

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CC of the nucleic acid are useful as probes or primers and to synthesise CC full length das polynucleotides. The nucleic acid and protein are useful CC for diagnosing bacterial infections, especially by Pseudomonas CC aeruginosa, stagling a disease or response of an infectious organism to CC drugs, and are also used in a structure based design of an (ant) agonist to das, The nucleic acid, protein and antibodies raised against it are CC useful for screening for (ant) agonists of dax or the nucleic acid and are useful to interfere with the initial physical interaction between a CC pathogen and a mammalian host responsible for sequelae of infection. CC These molecules are useful in preventing adhesion of gram positive and/or CC gram negative bacteria to eukaryotic extracellular matrix proteins or in-dwelling devices or in wounds; to block bacterial adhesion; to block the normal progression of pathogenesis in infections initiated other than CC the implantation of in-dwelling devices or by other surgical CC infection, and also useful for identifying membrane bound or soluble receptors. The (ant) agonists are useful for treating Helicobacter pylori infection, and also to prevent, inhibit or treat gastric ulcers, CC gastritis and gastrointestinal carcinoma.

CC from the dxs sequence is not shown in the specification but is derived CC from the dxs sequence given in AAU00012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The sequence represents Pseudomonas aeruginosa deoxyxylulose-5-phosphate synthase, dxs, temperature sensitive mutant (st-32. (Ant)agonists of dxs are useful for treating an individual in need of enhanced or inhibited activity or expression of or immunological response to dxs. Dxs and the nucleic acid encoding it are useful as diagnostic reagents, especially in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page - ; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New deoxyxylulose-5-phosphate (dxs) polypeptides of Pseudomonas aeruginosa useful for diagnosis of dxs expression or activity related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relation to diseases related to expression or activity of dxs. Fragments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2001-211303/21
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밁 δ ₽ S 문 Ś 문 S 밁 5 밁 Ś 뮹 δ Matches Query Match Best Local : 426 196 188 387; 76 89 16 00 Similarity PDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQHHGPASVRYPRGKGFGAAI VAIAEQHAVTLAAGMACEGMKPVVAIYSTFLQRAYDQLIHDVAVQHLDVLFAIDRAGLVG VAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVG NYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPTK AALGWAIASQLRGEDKKWVAIIGDGSITGGMAYEAMUHAGDVNANLLVILNDNDMSISPP LEAPGSAPKKTGGPKYSSVFGQWLCDMAAQDARLLGITPAMKEGSDLVAFSERYPERYFD DELPKAAP--SPHPTYTEVEGRWLCDWAAQDERLLGITEAMREGSGLVEFSQKFPNRYFD NYIGPIDGHDLPTLVATLRNMRDMKGPQFLHVVTKKGKGFAPAELDPIGYHAI----VGGLSNYLAKILSSRTYSSMREGSKKVLSRLPGAWEIARRTEEYAKGMLVPGTLFEELGW VGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELGP TPDDRLVWDVGHQAYPHKILTERRELMGTLRQKNGLAAFSRRAESEYDTFGVGHSSTSIS TPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSIS PLIKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVFN AALGMAIAARLQGKERKSVAVIGDGALTAGMAFEALNHASEVDADMLVILNDNDMSISHN 195 PLIDRASSPAELERLGEADLETLADELRQYLLYTVGQTGGHFGAGLGVVELTIALHYVFD Conservative 100; 64.1%; Score 2061.5; DB 2; Pred. No. 9.3e-180; DO; Mismatches 118; DB 22; Indels Length 627 7; Gaps 485 430 425 307 370 365 310 255 247 135 127 75 2

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RESULT 8
AAU38490
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The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antiblotics, the essential genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella pneumoniae, Pseudomonas aeruginosa and Enterococcus faccalis. The promotion is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. The proteins can be used to scene nucleic acid sequence is also useful to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an cessential prokaryotic cellular proliferation protein.
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27-NOV-2000; 2
72-DEC-2000; 7
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23-MAY-2000;
26-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Antisense; prokaryotic cellular proliferation antibiotic; antibacterial; drug design.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polynucleotides for the identification and development biotics, comprise sequences of antisense nucleic acids
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B; AAS56349.
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                                                   MAAQHDALVIILBENA IMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQEEARABLG
                                                                               LARTHDVFVTVBBNVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
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                                                                                                                                                                                  DGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQHH-GPASVRYPRGKGFGAAI
                                                                                                                                                                                                                                       AIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVGP
                                                                                                                                                                                                                                                                              SGCLPKSS-GGLPGYSKIPGDWLCETAAKDSKLMAITPAMREGSGMVEFSRKFPDRYFDV
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                         LDSKGILATIEQFCA
                                                                                                                                      DPTLTALEIGKAEVRHIGSRIAILAWGSMVTPAVEAGKQLGATVVMYRFVKPFDQALVLE
                                                                                                                                                                                                                       AIAEQHAVTFAAGLAIGGYKPVVAIYSTFLQRAYDQVIHDVAIQKLPVMFAIDRAGIVGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI
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Pred. No. 1.9e
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L.9e-175;
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AAY52832 standard; Protein; 620 Ã

AAY52832;

26-JAN-2000 (first entry)

Escherichia 011 protein sequence SEQ Ħ NO:1.

RESULT 9
AAY52832
ID AAY52
ID AAY5
AC AAY5
AC AAY5
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AC AAY5
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ISOP
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ISOP Isoprenoid; microorganism; detection; antibacterial; herbicide; heart disease; osteoporosis; haemostasis; cancer; immunopotentiation; health food; antifouling coating; farnesyl pyrolinic acid; pyruvic acideoxy-D-xylulose-5-phosphate; glycerylaldehyde-3-phosphate; 2-C-methyl-D-erythreitol-4-phosphate. Escherichia coli acid,

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                                                                                                                                                                                                                                                                                                                                                                                                                                             CC compound comprising using at least 1 DNA e.g. encoding a farnesyl CC pyrolinic producing enzyme. The method of preparation of an isoprenoid CC pyrolinic producing enzyme. The method of preparation of an isoprenoid CC pyrolinic producing enzyme. The method of preparation of an isoprenoid CC pyrolinic producting enzyme. The method of preparation of an isoprenoid CC compound comprises using at least 1 DNA, a vector, cloned cells, their CC derived recombinant DNAs or transformed products in a culture system and CC exitating the isoprenoid accumulated in the medium. The DNA encodes at CC least 1 of the following; (a) a compound for activating or catalysing CC the production of 1-deoxy-D-xylulose-5-phosphate from pyruvic acid and CC glycerylaidehyde-3-phosphate; (b) an enzyme producing farnesyl pyrolinic CC acid; (c) a protein which elevates the efficiency of synthesis of CC isoprenoid compounds and comprises a 3 or 4 amino acid sequence CC gibstituted or an additional amino acid being inserted; (d) a protein which activates or catalyses the production of 2-C-methyl-D-crythreitol-CC 4-phosphate from 1-deoxy-D-xylulose-5-phosphate; or (e) a protein which activates a target compound or reaction and is a string end or hybrid of CC the DNA encoded in (a)-(e). Isoprenoid compounds are useful in drugs CC (e.g. for the treatment of heart diseases, osteoporosis and hemostatis, CC on the non-mevalonate pathway and can be used as antibacterials and CC on the non-mevalonate pathway and can be used as antibacterials and CC herbicides. The present sequence is used in the exemplification of CC the processont invention.
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Matches 370
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05-AUG-1998;
15-FEB-1999;
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N-PSDB; AAZ33157.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Preparation of recombinant isoprenoid compounds useful for treatment heart diseases, osteoporosis and hemostatis, preventing cancer and
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FNYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPT
                                                                                                                                                                                            NTPFDQLIWDVGHQAYPHKILTGRRDKIGTIRQKGGLHPFPWRGESEYDVLSVGHSSTSI
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                                                                                       LARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
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LDAAGMEAKIKAWLA
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RESULT 10 AAY08880 AAYO8880; AAY08880 standard; protein; 620 A

DXS protein

13-AUG-1999

(first

1-deoxy-D-xylose-5-phosphate synthase; DXS; modulator; pyruvate; glyceraldehyde-3-phosphate; GA3P; 1-deoxy-D-xylulose-5-phosphate; DXP structural analogue; pesticide; antibacterial; herbicide; biosynthesi: growth promoter; DXP derivative; isoprenoid; carotenoid; chlorophyll; phytol; lutein; sterol; ubquinone; rubber; taxane -phosphate; DXP; de; biosynthesis;

Escherichia coli

DE29800547-U1

08-APR-1999

16-JAN-1998; 98DB-2000547

28-NOV-1997; 97DB-1052700

(KERJ) FORSCHUNGSZENTRUM JUELICH GMBH HOECHST-SCHERING AGREVO GMBH.

WPI; 1999-230818/20

1-Deoxy-D-xylulose-5-phosphate synthase protein and modulators potentially useful as pesticides, antibacterial agents, herbic herbicides,

Claim رب ۰, Page 10; 21pp; German.

This invention describes a 1-deoxy-D-xylulose-5-phosphate synthase (DXS) protein or active fragment and a DXS modulator. The DXS modulator is a structural analogue of pyruvate, glyceraldehyde-3-phosphate (GA3P) or 1-deoxy-D-xylulose-5-phosphate (DXP). Compounds that inhibit DXS activity are potentially useful as pesticides, antibacterial agents or herbicides. Compounds that stimulate DXS activity are potentially useful as growth promoters or for increasing biosynthesis of DXP derivatives, especially isoprenoids such as carotenoids, chiorophyll, phytols, lutein, sterols, ubdquinone, rubber and taxanes.

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RESULT 11

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isoprenoid
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                                                                                                                                                                                                                                                                                                                  AAB20544 standard; protein;
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Manipulating isoprenoid expression in cells or organisms and identifying modulators of the expression, for use in antibacterials herbicides and to produce transgenic plants with improved properties HOLLOWAY & BEDFORD 99GB-0001902 NEW COLLEGE. properties

and

expression in cells or organisms having a mevalorate independent isopentyl diphosphate (IPP) synthesising pathway. The method comprises altering the activity of 1-deoxy-D-xylulose-5-phosphate synthase (DXPS) or a functional equivalent, derivative, or bioprecursor of it. The isoprenoid activity or expression modulators are used as medicaments to treat bacterial diseases, and as herbicides. The method can be used to produce transgenic plants which have higher levels of isoprenoids, and which have health care benefits when consumed. The present sequence represents the DXPS protein from Escherichia coli, which is used in the exemplification of the present invention. The present invention describes a method for manipulating isoprenoid (DXPS) ť

Length

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LARTHDVFVTVBENVIAGGAGSAINTFLQAQXVLMPVCNIGLPDRFVEQGSREELLSLVG
                                                                                 KDFLPKAAPSPHPTYTEVPGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRYFDV
MAASHEALVTVEENAIMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQBEMRAELG
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Pred. No. 3.6e-174;
4; Mismatches 128;
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01-OCT-1998;
01-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes the novel use of a DNA sequence encoding 1-deoxy-D-xylulose-5-phosphate synthease (DNAS), and optionally p-hydroxyphenylpyruvate dioxygenase (HPPD) and/or geranylgeranyl-pyrophosphate oxidoreductase (GGPPOR), to produce a plant with increased tocopherol, vitamin K, chlorophyll and/or carotenoid content. Transgenic plants containing DOXS DNA coding sequences can be used for production of plant and bacterial DOXS which also have increased tocopherol, vitamin K, chlorophyll and/or carotenoid content. The test system can be used to identify inhibitors of DOXS. This sequence represents the Escherichia coli DOXS protein described in the method of the invention.
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98DE-1045231.
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1.6e-174;
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23-MAY-2000; 2000US-206848P.
26-MAY-2000; 2000US-207727P.
23-OCT-2000; 2000US-242578P.
27-NOV-2000; 2000US-253625P.
22-DEC-2000; 2000US-25931P.
16-FEB-2001; 2001US-269308P.
New polynucleotides for the identification and development antibiotics, comprise sequences of antisense nucleic acids
                                                                                              WPI; 2001-611495/70
                                                                                                                                              Haselbeck R,
Yamamoto RT,
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c. prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antibiotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are CC Bscherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets for antibiotic development. The antisense mucleic acids can also be used to identify proteins used in proliferation, to express these proteins, CC and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence represents an CCC essential prokaryotic cellular proliferation protein.

CC Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic CCC format directly from WIPO at
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Matches 370;
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                                                                                      LARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
                                                                                                                                    TP-LEKLPIGKGIVKRRGEXLAILNFGTLMPEAAKVAESLNATLVDMRFVKPLDEALILE
                                                                                                                                                                                                                                                                                              AIASQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVGP
                                                                                                                                                                                                                                                                                                                                                                  KDFLFKAAPSPHETYTEVEGRWLCDMAAQDERLLGITFAMREGSGLVEFSQKFPNRYFDV
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LDAAGMEAKIKAWLA 620
                                                                   MAASHEALVTVEENAIMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQEEMRAELG
                                                                                                                                                                     DPTLTALBIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                                                                                                                                                                                      DGQTHQGAFDLSYLRCIPEMVINTPSDENECRQMLYTGYHYNDGPSAVRYPRGNAVGVEL:
                                                                                                                                                                                                                                 DGPTHAGAFDYSYMRCIPNMLINAPADENECROMLTTGPOHH-GPASVRYPRGKGPGAAI
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                               LDSKGILATIEQFCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                   FNYFGPIDGHDVEMIVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPT
                                                                                                               NVGALNNHLAQLLSGKLYSSLREGGKKVFSGVPPIKELLKRTEEHIKGMVVPGTLFEELG
                                                                                                                                            PVGAMMYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELG
                                                                                                                                                                                                                                                                                                                                  NTPFDQLIWDVGHQAYPHKILTGRRDKIGTIRQKGGLHPFPWRGESEYDVLSVGHSSTSI
                                                                                                                                                                                                                                                                                                                                                                                                                                            YPTLALVDSTQELRLLPKESLPKLCDBLRRYLLDSVSRSSGHPASGLGTVBLTVALHYVY
FWYIGPVDGHDVLGLITTLKNWRDLKGPQFLHIMTKKGRGYEPAEKDPITFHAVPKFDPS
                                                                                                                                                                                                                                                                          SAALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISP 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jessen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     620 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114;
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Pred. No. 3.6e-174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                          The invention relates to methods and materials for the production of isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS) activity, is useful for increasing production of CoQ(10) in a cell having endogenous DDS activity. This sequence represents a protein relating to the isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                      production of the
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 6; 246pp;
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1: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2 6/ptodata/1/pubpaa/PCT NEW PUB.pep:*

3: /cgn2 6/ptodata/1/pubpaa/US06 NEW PUB.pep:*

4: /cgn2 6/ptodata/1/pubpaa/US06 PUBCOMB.pep:*

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6: /cgn2 6/ptodata/1/pubpaa/US07 PUBCOMB.pep:*

7: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

8: /cgn2 6/ptodata/1/pubpaa/US08 NEW PUB.pep:*

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9 US-09-815-242-10068

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Sequence 2, Appli
Sequence 6, Appli
Sequence 13998, A
Sequence 15, Appl
Sequence 14083, A
Sequence 21174, A
Sequence 21174, A
Sequence 31, Appl
Sequence 31, Appl
Sequence 15911, A
Sequence 15281, A
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1985.5 61.7 616 12 US-10-369-493-4669 Sequence 4669, Ap 1997.1 61.3 615 12 US-10-369-493-9272 Sequence 9272, Ap 1967.6 61.2 613 12 US-10-369-493-9367 Sequence 9272, Ap 1967.6 61.2 613 12 US-10-369-493-9367 Sequence 9367, Ap 1975.6 62.2 625 12 US-10-381-779-32 Sequence 33, Appl 1776.5 62.6 624 12 US-10-381-779-32 Sequence 32, Appl 1620.5 50.4 628 12 US-10-381-779-18 Sequence 10188, A 1620.5 50.4 628 12 US-10-381-779-19 Sequence 61, Appl 1620.5 50.4 628 12 US-10-369-493-10188 Sequence 61, Appl 1532.5 48.0 637 12 US-10-369-493-1290 Sequence 20596, A 1532.5 47.7 641 12 US-10-369-493-1290 Sequence 20596, A 1532.5 47.4 640 12 US-10-369-493-16942 Sequence 10188, A 1523.5 47.4 640 12 US-10-369-493-16942 Sequence 101848, A 1523.5 47.6 629 12 US-10-369-493-16942 Sequence 101848, A 1523.5 46.6 634 12 US-10-369-493-11753 Sequence 10842, A 1649.5 46.6 635 12 US-10-369-493-11753 Sequence 11753, A 1649.5 46.6 635 12 US-10-369-493-11753 Sequence 26, Appl 1644 44.9 671 12 US-10-369-493-10317 Sequence 27, Appl 1644 44.9 671 12 US-10-369-493-10317 Sequence 29, Appl 1644 44.8 640 12 US-10-369-493-10316 Sequence 29, Appl 1646 44.7 64.8 64.0 12	4. TU	44	43	42	41	40	3	86	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	. 19	18	17	٠ <u>٩</u>
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ALIGNMENTS

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                                                                                                                                                            ; ORGANISM: Methylomonas 16a; FEATURS: OTHER INFORMATION: Amino acid sequences encoded by ORF1 US-09-934-903-2
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PRIOR FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOPTWARE: Microsoft Office 97
SEQ ID NO 2
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US-09-934-903-2
                                                                               Matches
                                                                                                      Best
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KOffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andreas J.
APPLICANT: No. US20020102690Alton,
APPLICANT: Tomb, Jean-Francois
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Picataggio, Stephen
APPLICANT: Cheng, Qiong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: CL1646 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
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                                                                          100.0%; Score 3216; DB 10; ilarity 100.0%; Pred. No. 1.1e-298; Conservative 0; Mismatches 0;
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Sequence 62, Application US/09934868

Patent No. US20020137190A1

GENERAL INFORMATION:

APPLICANT: Koffas, Mattheos

APPLICANT: Codom, James M

APPLICANT: Codom, James M

APPLICANT: Schenzle, Andreas J

TITLO OF INVENTION: DENITHIFYING METHANOTROPHIC BACTERIAL STRAIN

PILE REFERENCE: CLL596 US NA

CURRENT APPLICATION NUMBER: US/09/934,868

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Microsoft Office 97

SEQ ID NO 62

TYDE: DEN
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Best Local
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ALHYVFNTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDRLFALDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DMSISPPVGAVANYLTKVLSSKFYSSVREESKKALAKWPSVWELARKTBEHVKGMIVPGT
                                     MKLTTDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHPAAGLGTVELTV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGAAIDPTLTALBIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGLVGPDGPTHAGAPDYSYMRCIPNMLIMAPADENECROMLTTGPQHHGPASVRYPRGKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLITGFOHHGPASVRYPRGKG
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                                                                                                                Conservative
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                                                                                                          100.0%; Score 3216; DB 10; 100.0%; Pred. No. 1.1e-298; tive 0; Mismatches 0;
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APPLICANT: Miller, Edward S. Jr.
APPLICANT: Odom, J. Martin
APPLICANT: Picataggio, Steve
APPLICANT: Picataggio, Steve
APPLICANT: Rouviere, Pierre B.
FITTLE OF INVENTION: CAROTERVOID PRODUCTION FROM A SIN
FILE REFERENCE: CL1903 US NA
CURRENT APPLICATION NUMBER: US/09/941,947A
CURRENT APPLICATION NUMBER: 00/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR APPLICATION NUMBER: 60/229,907
                                                                                       ; LENGTH: 620
TYPE: PRT
; ORGANISM: Methylomonas 16a
US-09-941-947A-6
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US-09-941-947A-6
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             Query Match
Best Local Similarity
Matches 620; Conserv
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PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 6
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APPLICANT:
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DiCosimo, Deana J.
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             100.0%; Score 3216; DB 11; illarity 100.0%; Pred. No. 1.1e-298; Conservative 0; Mismatches 0;
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                                                                                                                            SEQ ID NO 13998
LENGTH: 628
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Query Match

Best Local Similarity 63.2

Matches 387; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13998, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                                                                                                   APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                           TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REPERIOE: 38-10 (52052) B CURRENT APPLICATION NUMBER: US/10/369,493 CURRENT FILING DATE: 2003-02-28 PRIOR APPLICATION NUMBER: US 60/360,039 PRIOR PILING DATE: 2002-02-21 NUMBER OF SEQ. ID NOS: 47374
                                                                                        TYPE: PRT
ORGANISM: Pseudomonas
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64.7%; Score 2080; DB 1
63.2%; Pred. No. 7e-190;
tive 101; Mismatches 12
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                                  DB 12;
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                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID NCS: 190
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-10-381-779-15
; Sequence 15, Application US/10381779
; Publication No. US20030219798A1
                                                                      US-10-381-779-15
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Query Match

G4.4%; Score 2069.5

Best Local Similarity 63.4%; Pred. NO. 7.1e

Matches 388; Conservative 100; Mismatches
                                                                                      LENGTH: 627
TYPE: PRT
ORGANISM: Pseudomonas
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es 117;
                                    DB 12;
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RESULT 6
US-09-815-242-14083
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    CURRENT APPLICATION NUMBER: US/09/815,24
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14083, Application US/09815242 Patent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                  APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
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                                                                                                                                                                                                                                                                                                                                            Ohlsen, Kari L.
Zyskind, Judith W.
Wall, Daniel
Trawick, John D.
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| UGGLSNYLAKILSSRTYSSMRBGSKKYLSRLPGAWEIARRTBBYAKGMLVPGTLFEBIGW 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DFLFKAAP--SPHFTYTSVFGRWICDMAAQDERLLGITFAMREGSGLVEFSQKFPNRYFD 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYIGPIDGHDLFTLVATLRNMRDMKGPQFLHVVTKKGKGFAPAELDFIGYHAI-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLLDRASSPAELRRIGEADLETLADELRQYLLYTVGQTGGHFGAGLGVVELTIALHYVFD
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US-10-369-493-481
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US-09-815-242-14083
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LENGTH: 620
TYPE: PRT
                                                                                                                                  GENERAL INFORMATION:
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Best Local
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
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PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR ETILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRACESEQ for Windows Version
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Similarity 61.0%;
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Pred. No. 1.3e-183;
6; Mismatches 131;
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RESULT 8
US-10-369-493-21174
US-10-369-493-21174
Sequence 21174, Mg21030233675A1
Sequence 21174, Mg2030233675A1
Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Slater, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION (
DEANTS WITH IMPROVED PROPERTIES
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 481
LENGTH: 619
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                                                                                                       US-09-815-242-10068

Sequence 10068, Application US/09
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
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Best Local Similarity
Matches 377; Conserv
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CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21174
                                                                                            APPLICANT:
APPLICANT:
                                                            APPLICANT:
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TYPE: PRT
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                                                          Carr, Grant J.
Yamamoto, Robert
                                                                                          Trawick, John D.
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR PILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR PILING DATE: 2000-15-26
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR PILING DATE: 2000-11-27
PRIOR PILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10068
LENGTH: 620
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Best Local:
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ORGANISM: Escherichia
09-815-242-10068
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LDSKGILATIEQFCA 620
                                      LARTHDVFVTVEENVIAGGAGSAINTFLOAQKVLMPVCNIGLPDRFVEQGSREELLSLVG 605
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                                                                                                                 TP-LEKLPIGKGIVKRRGEKLAILNFGTLMPEAAKVAESLNATIVDMRFVKPLDEALILE
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ilarity 60.2%;
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Pred. No. 2.8e-182;
4; Mismatches 128;
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APPLICANT: Jessen, Holly
APPLICANT: Jiessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
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Best Local S
Matches 370
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SEQ ID NO 31
LENGTH: 620
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Publication No.
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                                      MAASHEALVIVEENAIMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQEEMRAELG
                                                                                                                 TP-LEKLPIGKGIVKRRGEKLAILNEGTLMPEAAKVAESLNATLVDMREVKPLDEALILE
                                                                                                                                                   DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
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LDAAGMEAKIKAWLA
  LDSKGILATIEQFCA
                                                                            LARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
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o. US20030219798A1
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Pred. No. 2.8e-182;
14; Mismatches 128; I)
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Indels

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Gaps

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127 126

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545

486 485 426

808 605 545 426

366

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247 246

307

366

Length 620;

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 731
LENGTH: 620
TYPE: PRT
CRANISM: Escherichia coli
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Matches 370
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APPLICANT: Hink
APPLICANT: Slat
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                          TP-LEXLPIGKGIVKRRGEKLAILNEGTLMPEAAKVAESLNATLVDMREVKPLDEALILE
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LDSKGILATIEQFCA
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o. US20030233675A1
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2.8e-182;
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US-10-369-493-15911
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US-10-369-493-15911
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gre
APPLICANT: Siater, Ste
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PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15911
LENGTH: 623
TYPE: PRT
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Publication No. US20030233675A1
GENERAL INFORMATION:
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APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)8
FULL REFERENCE: 38-10(52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
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KAMLLELAKCHEAFVSIEDNVVAGGAGSGVSELLNAESVLMPMLHLGLPDSFQHHASRED
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                                                       QALVLBLARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREE 599
                                                                                                                                                                   GPGAAIDPTLTALBIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFD 539
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                                                                                                                     GPGTALDASLTTLPIGKAQLRHSGARIALLGFGATVDAAEAVGRELGLTVVNMRFVKPLD
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Pred. No. 1.7e-181;
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US-10-369-493-16281
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APPLICANT: Cao, Yongwei

APPLICANT: Hinkle, Gregory J.

APPLICANT: Slater, Steven C.

APPLICANT: Coldman, Barry S.

FILE REFERENCE: 38-10 (52052)B

CURRENT APPLICATION NUMBER: US 50/369,493

CURRENT FILING DATE: 2003-02-28

PRIOR FILING DATE: 2003-02-29

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR FILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

LENGTH 623
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Publication No. US20030233675A1
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US-10-369-493-15540
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 15540
LENGTH: 653
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROFEINS IN PLANTS ITTLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 2003-02-28
CURRENT FILING DATE: 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 - 100 
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Similarity 61.4%;
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GENERAL INFORMATION:
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (5-2052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT PILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 7428
LENGTH: 619
TYPE: PRT
ORGANISM: Burkholderia cepacia
US-10-369-493-7428
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US-10-369-493-7428
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                                              VATIKOMTALPLGKGEIRRETSOPAGKRIAILAFGTMVAPSLAAAEQLDATVANMRFVKP
                                                                      AAIDPTLTALEIGKAEVRHH-----GSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKP 537
                                                                                                                                    UGADGATHAGAYDLAFLRCIENMTVMAASDENECROMLYTALQQPNETAVRYERGAGTG
                                                                                                                                                                           LVGEDGETHAGAFDYSYMRCIENMLIMAFADENECRQMLTTGFQHHGFASVRYFRGKGEG 482
                                                                                                                                                                                                                              YFDVGIAEQHAVTFAGGLAAEGMKEVVAIYSTELQRAYDQLIHDVALQNLEVVFAIDRAG
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Db 542 LDADLURQLAETHDAIVIVEEGCVMGGAGSACVEALLASGVTRPVLQLGLPDRFIDHGDP 601

Qy 598 BELLSLVGLDSKGILATI 615

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602 AKLLAACGIDAVGITKSI 619
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Search completed: January 29, 2004, 16:21:14 Job time: 44.3225 secs

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US-09-626-589-1
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	49, Appl	3422, Ap	54, Appl	32382, A	45, Appl	46, Appl	5240838	3207, Ap	4640, Ap	44 Appl	Appli	6441, Ap	4298, Ap	19811, A	2, Appli	16, Appl	966, App	5219, Ap

ALIGNMENTS

RESULT 1 US-09-252-991A-26388

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: ARRUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: 107196.136
CURRENT PELLING DATE: 1999-02-18
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-16
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26388
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GENERAL INFORMATION:
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Best Local
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TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
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64.4%; Score 2069.5; DB 4;
Local Similarity 63.4%; Pred. No. 4e-199;
hes 388; Conservative 100; Mismatches 117;
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                                                                                                                                            VGGLSNYLAKILSSRTYSSMREGSKKVLSRLPGAWEIARRTEEYAKGMLVPGTLFEELGW
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GENERAL INFORMATION:
APPLICANT: GARY L. Breton et al.
APPLICANT: GARY L. BUCLEIC ACID AND AMINO ACID SEQUE
ITILE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THE
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION UNMEER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 6210
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Patent No. 6562951
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                                                    IAEQHAVTLAAGMACEGLXPVVAIYSTFLQRGYDQLIHDVALQNLDVTFGIDRAGLVGED
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                                                                                                                                                                                                            DYFGPFDGHDVTQLVQVFNALKKRKGPRLVHVYTKKGKGFAPABADPITYHAIGKINAA-
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                                                                                        IAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVGPD
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LENGTH: 720
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CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,779
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
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APPLICANT: Yong Tao
APPLICANT: Zude Weng
APPLICANT: Mark E. Williams
TITLE OF INVENTION: Plant 1-Deoxy-Xylulose
FILB REFERENCE: BB1290
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TYPE: PRT
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  LDMLFALDRAGLYGPDGFTHAGAFDYSYMRCIPNMLIMAPADENE-CRQMLTTGFQHHGP 470
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HWQMLQDCGLDAKGILNSIER 639
                                                            LNYFLRRFPNRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFLQRGYDQVVHDVDLQK 487
                                                                                                                                                                          PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG
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APPLICANT: Zude Weng
APPLICANT: APPLICANT: Mark B. Williams
ITITLE OF INVENTION: plant 1-Deoxy-Xylulose 5-Phosphate Syn
FILE REFERENCE: BB1290
CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,779
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 34
LENGTH: 594
TYPE: PRT
ORGANISM: Oryza sativa
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  RAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENE-CROMLTTGFQHHGPASVRYPRG 478
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RDLKGGKNNVVAVIGDGAMTAGQAYEAMNNAGYLDSDMIVILNDNKQVSLPTATLDGPAP 182
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                                                                                                   PNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALD
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Yong Tao
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US-09-857-556A-12
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US-09-857-556A-12
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PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
LENGTH: 708
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Best Local :
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APPLICANT: Mark E. Williams
APPLICANT: Mark E. Williams
TITLE OF INVENTION: Plant 1-Deoxy-Xylulose 5-Phosphate Synthase
FILE REFERENCE: BB1290
CURRENT APPLICATION NUMBER: US/99/857,556A
CURRENT FILING DATE: 2001-06-04
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ASVRYPRGKGPGAAIDFT---LTALEIGKAEVRHHGSRIAILAWGSMYTPAVEAGK----
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                                                              LPVRPAMDRAGLVGADGPTHCGSPDVTFMACLPNMVVMAPSDEADLFHMVATAAAINDRP
                                                                                             LDMLFALDRAGLVGPDGPTHAGAPDYSYMRCIPNMLIMAPADENECRQMLTTGPQ-HHGP 470
                                                                                                                                            MNLFHRRFPTRCPDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFMQRAYDQVVHDVDLQK 479
                                                                                                                                                                                                                           ADKYHGVTKFDPPTGKQFKSKATTQSYTTY---FAEALIABAEADKDVVAIHAAMGGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGLGMAVGRDLKGRKNINVVAVIGDGAMTAGQAYEAMINIAGYLDSDMIVILINDNKQVSLPT
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46.9%; Pred. No. 9.5e-134;
ative 113; Mismatches 187; Indels 39,
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US-09-146-221-6
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US-09-146-221-6
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GENERAL INFORMATION:
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Best Local Similarity
Matches 298; Conserv
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APPLICANT: Lange, Bernd M
APPLICANT: Wildung, Mark R
APPLICANT: McGaskill, David G
TITLE OF INVENTION: Nucleic and Amino Acid Sequences Relating to a No. 61:
TITLE OF INVENTION: Transketclase, and Methods for the Expression Thereof
FILE REFERENCE: No. 6190895el transketclase from peppermint
CURRENT APPLICATION NUMBER: US/09/146,221
CURRENT FILING DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 60/056,033
EARLIER FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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VRYPRGKGPGAAIDPTL--TALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQL-----
                                                                                     MLFALDRAGIVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROML-TTGFQHHGPAS
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                                                                                                                                                                                       EFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLD 413
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46.9%; Pred. No. 1.66
tive 116; Mismatches
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; LENGTH: 72
; TYPE: PRT
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CURRENT FILLNS DATE: 1998-09-01
EARLIER APPLICATION NUMBER: 60/056,033
EARLIER FILLNS DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 12
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APPLICANT: Lange, Bernd M
APPLICANT: Wildung, Mark R
APPLICANT: McCaskill, David G
TITLE OF INVENTION: Nucleic and Amino Acid Sequences Relating to a No. 6190895el
TITLE OF INVENTION: Transketolase, and Methods for the Expression Thereof
FILE REFERENCE: No. 6190895el transketolase from peppermint
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5. 6190895
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  VRYPRGKGPGAAIDFTL--TALEIGKAEVRHGSRIAILAWGSMYTPAVEAGKQL-----
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                                                               VREWNDRAGVVGADGETHCGAEDTTYNACLENNVVMAESDEAELMNMIATAAIIDDRESC
                                                                                     MLFALDRAGIVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQML-TTGFQHHGPAS
                                                                                                                                                                                   EFSOKFPWRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLD 413
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                                                                                                                                                                                                                              -AKTGKOMKTKOKTKSÝTOYFAESÍVAEAEHDDKIVAÍHAAMGGGTGLN
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US-09-626-589-2
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SEQ ID NO 2
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CURRENT FILING DATE: 2000-07-27
NUMBER OF SEQ ID NOS: 6
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APPLICANT: Stewart, Sandy
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: INDENTIFICATION OF MODULATORS OF DECXYXYLULOSE 5-PHOSPHATE
TITLE OF INVENTION: SYNTHASE ACTIVITY
FILE REFERENCE: 2037 US
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   ASVRYPRGKGPGAAIDP--TLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAG-----K
                                                           LPVRFAMDRAGLVGADGPTHCGAFDVTFMACLPNMIVMAPSDEADLFNMVATAVAIDDRP
                                                                                LDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQ-HHGP 470
                                                                                                                                                                  LVBFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
                                                                                                                                                                                                                                       PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG 351
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                                                                                                                                                                                                                                                                                           -VPGTLFEELGFNYFGFIDGHDVEMLVSTLENLKD--LTGPVFLHVVTKKGKGYAPAEKD 293
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Kloti, Andreas
Crawford, John
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                                                                                                                              LNLFQRRFFTRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFMQRAYDQVVHDVDLQX
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46.6%; Pred. No. 6.8e-133;
tive 115; Mismatches 188;
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APPLICANT: Crawford, John
APPLICANT: Crawford, John
APPLICANT: Crawford, John
APPLICANT: Lamning, Beth
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: INSENTIFICATION OF MODULATORS OF DEOXYXYLULOSE 5-PHOSPHATE
TITLE OF INVENTION: SYNTHASE ACTIVITY
FILE REFERENCE: 2037 US
CURRENT APPLICATION NUMBER: US/09/626,589
CURRENT APPLICATION NUMBER: US/09-626,589
CURRENT APPLICATION HOMBER: 2000-07-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 717
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Best Local Similarity
Matches 297; Conserv
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471 ASVRYPRGKGPGAAID?--TLTALEIGKAEVRHHGSRIAILAMGSMVTPAVEAG----
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                                                       LPVRFAMDRAGIVGADGPTHCGAPDVTFMACLPNMIVMAPSDEADLFNMVATAVAIDDRP
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                                                                                                                                                                                                                          PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDEKLLGITPAMREGSG
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                                                                                         LDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQ-HHGP 470
                                                                                                                                LNLFQRRFPTRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFMQRAYDQVVHDVDLQK
                                                                                                                                                                                                   DDKYHGVVKFDPATGRQP----KITNKTQSYTTYPAEALVAEAEVDKDVVAIHAAMGGGTG
                                                                                                                                                                                                                                                                           GTGSSLFEELGLYYIGPVDGHNIDDLVAILKEVKSTRTTGPVLIHVVTEKGRGYPYAERA 374
                                                                                                                                                                                                                                                                                                        -VPGTLFBELGFNYFGPIDGHDVEMLVSTLENLKD--LTGPVFLHVVTKKGKGYAPAEKD 293
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CURRENT FILING DATE: 2000-07-27
RUMBER OF SEQ ID NOS: 6
SOFTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 824
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Rice, John
APPLICANT: Kloti, Andreas
APPLICANT: Crawford, John
APPLICANT: Crawford, John
APPLICANT: Lanning, Beth
APPLICANT: Stewart, Sandy
TITLE OF INVENTION: EXTREDS AND COMPOSITIONS FOR THE
TITLE OF INVENTION: INDENTIFICATION OF MODULATORS OF DEOXYXYLULOSE 5-PHOSPHATE
TITLE OF INVENTION: SYNTHASE ACTIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
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No. 6326164
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  LDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQ-HHGP
                                                                                 LVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
                                                                                                                                                                       PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG
                                                                                                                                                                                                                                                                                                         ATTLDGPSPPVGALSSALSRLQSNPALRELREVAKGMTKQIGGPMHQLAAKVDEYARGMIS
                                                                                                                               DDKYHGVVKFDPATGRQF----KTTNKTQSYTTYFABALVABABVDKDVVAIHAAMGGGTG
                                                                                                                                                                                                                                                 -VPGTLFEELGENYFGPIDGHDVEMLVSTLENLKD--LTGPVFLHVVTKKGKGYAPAEKD 293
                                                                                                                                                                                                                                                                                                                                                                                                                                         AALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDN-DMSI-- 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVFN
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                                                                                                                                                                                                                                                                                                                                                                                             AGLGMAVGRDLKGKUNNVVAVIGDGAMTAGQAYBAMNVAGYLDSDKIVILNDNKQVSLPT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TPQDKILWDVGHQSYPHKILTGRRGKMPTMRQTNGLSGFTKRGESEHDCFGTGHSSTTIS 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPVDQLVWDVGHQAYPHKILIGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSIS 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLLDTINYPIHMKNLSVKELKQLSDELRSDVIFNVSKTGGHLGSSLGVVELTVALHYIFN 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --MPVCNIGLPDRFVEQGSREELLSLVGLDSKGILAT 614
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US-09-857-556A-10
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LENGTH: 721
TYPE: PRT
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APPLICANT: Zude Weng
APPLICANT: Mark E. Williams
TITLE OF INVENTION: Plant 1-Deoxy-Xylulose 5-Phosphate Synthase
FILE REFERENCE: BB1290
CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/110,779
PRIOR APPLICATION NUMBER: 60/110,779
PRIOR FILING DATE: 1998-12-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rebecca E. Cahoon APPLICANT: Sean J. Coughlan APPLICANT: Yong Tao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 136 APKDKILWDVGHQSYPHKILTGRRDKWHTMRQTDGLAGFTKRSESDYDCFGTGHSSTTIS
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LDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLFTGFQ-HHGP
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                                         MNLFLRRFPTRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFMQRAYDQVVHDVDLQK
                                                                               LVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN 411
                                                                                                                           ADKYHGVTKFDPATGKQFKSNÄÄTQSYTTY---FAEALIAEAEADKDIVGIHAAMGGGTG
                                                                                                                                                                     PLAYHGVPAPDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG
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47.0%; Pred. No. 1e-132;
tive 107; Mismatches 18
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APPLICANT: Zude Wang
APPLICANT: Mark E. Williams
ITITLE OF INVENTION: plant 1-Deoxy-Xylulose 5-Phosphate Synthase
FILE REFERENCE: BH1290
CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT APPLICATION NUMBER: US/09/857,556A
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 00/110,779
PRIOR FILING DATE: 1998-12-03
INUMBER: OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 33
LENGTH: 719
TYPE: PRT
ORGANISM: Capsicum annuum
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Patent No. 6558915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rebecca E. Cahoon APPLICANT: Sean J. Coughlan APPLICANT: Yong Tao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local 294;
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                                          MNLFLRRFPTRCFDVGIAEQHAVTFAAGLACEGLKPFCAIYSSFMQRAYDQVVHDVDLQK
                                                                                                                                                          PLAYHGVPAFDPT--KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSG
                                                                                                                                                                                                    GSGSTLFEELGLYYIGPUDGHNIDDLISILKEVRSTKTTGPVLIHVVTEKGRGYPYAERA 373
    LDMLFALDRAGLVGPDGFTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQ-HHGP
                                                                           LVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQN
                                                                                                                      ADKYHGVAKFDPATGKOFKGSAKTOSYTTY---FARALIARARADKDIVAIHAAMGGGTG
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                                                                                                                                                                                                                                        -VPGTLFEELGFNYFGPIDGHDVEMLVSTLENLKD--LTGPVFLHVVTKKGKGYAPAEKD 293
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APPLICANT: Lange, Bernd M
APPLICANT: Wildning, Mark R
APPLICANT: Wildning, Mark R
APPLICANT: McCaskill, David G
TITLE OF INVENTION: Nucleic and Amino Acid Sequences Relating to a No. 619089
TITLE OF INVENTION: Transketolase, and Methods for the Expression Thereof
FILE REFERENCE: No. 619085el transketolase from peppermint
CURRENT APPLICATION NUMBER: US/09/146,221
CURRENT FILING DATS: 1998-09-01
BEALIER APPLICATION NUMBER: 60/056,033
EARLIER APPLICATION SUMBER: 60/056,033
EARLIER FILING DATS: 1997-09-02
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 721
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; ORGANISM: Mentha piperita
US-09-146-221-4
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Best Local Similarity
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414 MLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROML-TTGFQHHGPAS
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                                                                                                                 ADKMHGVVKFD-AKTGKOMKTKNKTKSYTQYFAESLVABAEHDDKIVAIHAAMGGGTGLN 432
                                                                                                                                                       PLAYHGVPAFDPTKDFLPKAAPSPHPTYTEVFGRWLCDWAAQDERLLGITPAMREGSGLV 353
                                                                           EFSOKFPURYFDVAIAEQHAVTLAAGQACQGAKPVVAIYSTFLORGYDQLIHDVALQNLD 413
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                                        IFQKQFPDRCFDVGIAEQHAVTFAAGMAAEGLKPFCAIYSSFLQRGYDQVVHDVDLQKLP
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SEQ ID NO 1135
LENGTH: 644
TYPE: PRT
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APPLICANT: Griffais,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment: TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev. TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Chlamydia
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GAAIDPTLTA-----LEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQL-----GATVVN
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                                                                                                            RFFDVGIAEGHAVTFSAGIAKAGNPVICSIYSTFLHRALDNVFHDVCMQDLPVIFAIDRA
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                                              GLAYGDGRSHHGIYDMSFLRAMPQMIICQPRSQVVFQQLLYSSLHWSSPSAIRYPNIPAP
                                                                                                                                                                                                       - FDPTKDETPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFFN
                                                                                                                                                                                                                                   EQFGLAYVGDIDGHNVKKLIPILQSVRNLPFPILVHVCTTKGKGLDQAQNNPAKYHGVRA
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Patent No. 6583266 GENERAL INFORMATION:
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~ "coal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: GATES, EDWARD R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0044/7125
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/311,731A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 4:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
TITLE OF INVENTION: RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SMITH APPLICANT: MAO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0
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VGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWBLA----RKTEEHVKGMIVPGTLFE
                                          ADGLAKAFELAGNRNRHVVAVVGDGALTGGMCWEALNNIAATERPVVIVVNDNGRSYAPT 273
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                                                                                             ALCMAIASQLRG-EDKKMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISPP 187
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                                                                                                                                                                                                                                                                                                                         274 IGGVADHLATLRUPAYERLLEKGRDALHSLPLIGQIAYRFMHSVKAGIKDSISPOLLFT 333
                                                                                                              482 GAAIDPTL---TALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQL-----GATVVNNK 533
                                                                                                                                    511 ITGSDGPSHNGMWDLSMLGIVPGMRVAAPRDAIRLREELGEALDVDDGPTAIRFP--KGD 568
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Search completed: January 29, 2004, 15:57:02 Job time : 21.4586 secs

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                                                                                             1-deoxy-D-xylulose
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Result No.

45	44	4 ω	42	4 ⊒	40	39	38	37	ω 6	35	34	33	32	31	30
886	1044.5	1072.5	1086.5	1087.5	1099.5	1106.5	1119.5	1148	1148	1227	1227.5	1259.5	1274.5	1326	1351
27.5	32.5	نن نا نا	33.8	33.8	34.2	34.4	34.8	35.7	35.7	38.2	38.2	39.2	39.6	41.2	42.0
580	640	632	643	638	618	618	656	644	644	615	630	703	809	629	609
N	N	N	N	N	N	N	N	N	Ŋ	Ŋ	N	N	N	N	N
A86834	F71527	E81684	H87038	E70528	B64564	H71946	T35408	A72002	A86623	E81451	B71276	D71420	A72213	G75390	AB1245
1-deoxyxylulose-5-	probable transketo	1-deoxyxylulose-5-	hypothetical prote	probable dxs prote	transketolase B -	1-deoxyxylulose-5-	probable transketo	1-deoxyxylulose-5-	transketolase [imp	1-deoxyxylulose-5-	probable transketo	hypothetical prote	1-deoxyxylulose-5-	1-deoxy-D-xylulose	D-i-deoxyxylulose

ALIGNMENTS

Qy 360 PNRYFDVAIAEQHAVTLAAGQACQGAKDVVAIYSTELQRGYDQLIHDVALQNLDMLFALD 419	OY 300 VPAFDPTKDFTLPKAAPSPHPTYTEVPGRWLCDMAAQDERLLGITPAMREGSGLVEFSOKF	QY 240 TLEEBLGENYPGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHG	Qy 180 NDMSISPPVGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPG	Qy 120 GHSSTSISAALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMMHAGDVNANLLVILND	Qy 60 VALHYVENTEVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGV ::	Qy 3 LITDYPLLKNIHTPADIRALSKDQLQQLADBVRGYLTHTVSISGGHFAAGLGTVELT	Query Match 65.2%; Score 2097.5; DB 2; Length 626; Best Local Similarity 62.5%; Pred. No. 2.8e-139; Matches 391; Conservative 109; Mismatches 117; Indels 9; Gaps	ry HBIJ GB:AB004173; GB:AB003852; NID:g9655341; ce: serogroup O1; strain N16961; biotype thetical protein C2814	H82266 1-decxyxylulose-5-phosphate synthase VC0889 [imported] - Vibrio cholerae (s [
ALD 419	QKF 359 ::: KEY 359	YHG 299 YHG 300	VPG 239	LND 179	LPGV 119 LSV 120	ELT 60	īps 3;	PIDN:AAF94051.1; GSPDB:GN001; El Tor	cholerae (strain N16961 & 02-Feb-2001

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C; Genetics:
A; Gene: dxs; PA4044
C; Superfamily: hypothetical protein
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A;Residues: 1-627 <STO>
A;Cross-references: GB:AE004821; GB:AE004091; NID:g9950236; PIDN:AAG07431.1; GSPDB:GN00!
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C;Accession: G83139
A;Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
LOIY, S.; Olson, M.V.
Nature 406, 959-964, 2000
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C;Species: Pseudomonas aeruginosa
C;Sate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
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                                                              VAIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGIVG 425
                                                                                                                                                   DFLFKAAP---SPHPTYTEVFGRWLCDMAAQDERLLGTTPAWREGSGLVEFSQKFPNRYFD
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C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: A10385
C;Access
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A;Molecule type: DNA
A;Residues: 1-619 <KUR>
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                                                                                                    AIAEQHAVTLAAGQACQGAKPVVAIYSTELQRGYDQLIHDVALQNLDMLFALDRAGLVGP
                                                                                                                                                                                           KDFLFKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRYFDV
                                                                                                                                                                                                                                                                                          FNYFGPIDGHDVEMIVSTIENLKDLTGPVF1HVVTKKGKGYADĀEXDPLAYHGVPAFDPT
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                         DGPTHAGAFDYSYMRCI PNMLIMAPADENECROMLTTGFOHHGPASVRYPRGKGPGAAID
                                                                        AIAEQHAVTFAAGLAIGGYKPVVAIYSTFLQRAYDQLIHDVAIQNLPVLFAIDRGGLVGA
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Pred. No. 1.7e-133;
5; Mismatches 139;
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S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF0554
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A; Residues: 1-620 < PAR>
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R;Parkhill, J
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DGPTHAGAFDYSYMRCIPNWLIMAPADENECRQMLTTGFQHH-GPASVRYPRGKGPGAAI
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Pred. No. 1.8e-133;
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C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_c
C;Accession: D64771
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli
A;Reference number: A64720; MUID:97426617; PMID:9278503
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A;Status: nucleic acid sequence not shown; translation A;Molecule type: DNA
A;Residues: 1-620 <BLAT>
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C;Superfamily: hypothetical protein C2814
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 DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                DGPTHAGAFDYSYMRCIPNMLIMAPADENECRONLTTGFOHH-GPASVRYPRGKGPGAAI
                                                                                                  AIAEQHAVTFAAGLAIGGYKPIVAIYSTFLQRAYDQVLHDVAIQKLPVLFAIDRAGIVGA
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M.; Col

D.J.; Mayhew K.; Apodaca,

O157:H7, s

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A;Molecule type: DNA
A;Residues: 1-620 <HAY>
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21158231; PMID:11258796

A;Accession: B90688

A;Status: preliminary
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C; Superfamily:
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Matches 368;
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N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
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                                                                                                                                                  DGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGPOHH-GPASVRYPRGKGPGAAI
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Pred. No. 4e-132;
15; Mismatches 129;
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C;Superfamily: hypothetical protein C2814
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A;Residues: 1-620 <STO.
A;Cross-references: GB:AE005174; NID:g12513276; PIDN:AAG54770.1; GSPDB:GN00145; UWGP:Z05
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
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MAASHEALVTVEENAIMGGAGSGVNEVLMAHRKPVEVLNIGLEDFFIPQGTQEEMRAELG
                                                                                                                                                                                                                                                                                                                                  AIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVGP
                                                                                                                                                                                                                                                                                                                                                                                               NYGALNNHLAQLISGKIYSSIREGGKKYFSGYPPIKELIKKTEEHIKGWYVPGTIFEEIG
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                                                                                                                                                        DPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                                                                                                                                                                                    DGQTHQGAPDLSYLRCIPEMVIMTPSDENECRQMLYTGYHYNDGPSAVRYPRGNAVGVEL
                                                                                                                                                                                                                                 DGPTHAGAFDYSYMRCIFNMLIMAPADENECROMLTTGFOHH-GPASVRYPRGKGPGAAI
                                                                                                                                                                                                                                                                                                     AIAEQHAVTFAAGLAIGGYKPIVAIYSTFLQRAYDQVLHDVAIQKLPVLFAIDRAGIVGA
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A; Cross references: GB; EE004037; GB: AE003849; NID: g9107394; PIDN: AAF85048.1; GSPDB: GN001 A; Experimental source: strain 9a5c R; Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Asriones, M.R.S.; Bueno, K.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H. as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000 A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigrenado, M.A.; Madeira, A.M.B. N.; Matsino, C.L.; Marques, M.V.; Martins, F. A; Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.B.; de Sa, R.G.; Santelli, R.V.; Sawasak A; Authors: da Silva, A.C.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.F.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A, Reference number: A59328
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A;Molecule type: DNA
A;Residues: 1-670 <SIM>
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A;Note: for a complete list of authors see reference number A59328 below
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                                                                                                                                                                                                                                                                                                                                   MSISPPYGAMNNYLTKVLSSKFYSSVREESKKALA--KMPSVWELARKTEEHVKGMIVPG 239
                                                                                                                                                                                                                                                                                                                                                                                                                       TSISAALGMAIASQLRGEDKKMVAIIGDGSITGGMAYEAMMHAGDVN--ANLLVILNDND 181
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                                                 VAPFDPQKGLIKAGAKK--QTYTDVFSEWLCDMAAVEPRILAITPAMREGSGLVRFSQEY
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59.3%; Pred. No. 5.9e-129;
ative 98; Mismatches 147;
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A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, X.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: B64172
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A; Residues: 1-625 <TIGR>
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;Species: Haemophilus influenzae
;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Sep-1999;Accession: B64172
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Best Local
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                                                                                                                                                             DPTKDFLPKAAPSPHPTYTEVPGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRY 363
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                                                                       FDVAIAEQHAVTFATGLAIGGYKPVVAIYSTFLQRAYDQLIHDVAIQNLPVLFAIDRAGI
                                                                                                                                                                                                                                                          ELGENY IGPVDGHNI DELVATLTNMRNLKGPQFLHI KTKKGKGYAPAEKDP I GEHGVPKF
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: B81978
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Nature 404, 502-506, 2000
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C;Superfamily: hypot
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A;Experimental source: serogroup A, strain Z2491
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-637 <PAR>
A;Cross-references: GB:AL162753;
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A; Accession: B81978
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C;Species: Neisseria meningitidis
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                                                                                                                                                                                                                                  NVLAQTHDYLVTLBENAIQGGAGSAVAEVINSSGKSTALLQLGLPDYFIPQATQQEALAD 603
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                                                + THE TABLE TO THE TENT OF T
                                                                                                                                                       PAMREGSGLVEFSQKFPNRYFDVAIAEQHAVTLAAGQACQGAKFVVAIYSTFLQEGYDQL 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AALGMAIASQLRGEDKXMVAIIGDGSITGGMAYEAMNHAGDVNANLLVILNDNDMSISPP 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPEDKLVMDVGHQSYPHKILTGRKNQMHTMRQYGGLAGFPKRCESEYDAFGVGHSSTSIG 124
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                                                                          IHDVALQNLDMLFALDRAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTT
                                                                                                                                                                                                              VKYHAVAN-----LPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAIT
                                                                                                                                                                                                                                                                                               SL---SLFENFGFRYTGPVDGHNVENLVDVLEDLRGRKGPQLLHVITKKGNGYKLAENDP
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        GFQHHGPASVRYPRGKGPGAAIDPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGK 523
                                                                                                                               PAMREGSGLVEFEORFFDRYFDVGIAEOHAVTFAGGLACEGMKPVVAIYSTFLORAYDOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TPVDQLVWDVGHQAYPHKILTGRKBRMPTIRTLGGVSAFPARDESBYDAFGVGHSSTSIS 127
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C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C;Accession: D81034
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A. Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve A;Reference mumber: A81000; MUID:20175755; PMID:10710307
A;Accession: D81034
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A,Molecule type: DNA
A,Residues: 1-637 <TET>
A,Crose-references: GB:AE002536;
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C; Superfamily:
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          GFOHHGPASVRYPRGKGPGAAIDPTLTALEIGKAEVRHHGSRIAILAMGSMVTPAVEAGK 523
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPEDKLVWDVGHQSYPHKILTGRKNQMHTMRQYGGLAGFPKRCESEYDAPGVGHSSTSIG
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                                                                        VHDIALQNLPVLFAVDRAGIVGADGPTHAGLYDLSFLRCVPNMIVAAPSDENECRLLLST
                                                                                                                                                                                    PAMREGSGLVEFSQKFPNRYFDVALAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQL 403
                                                                                                                                                                                                                                                                                                                       SL---SLPENFGFRYTGPVDGHNVENLVDVLKDLRSRKGPQLLHVITKKGNGYKLAENDP
                                                                                                                                                                                                                                                                                                                                                    MIVPGTLFEELGFNYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDP
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                                                                                                         IHDVALQNLDMLFALDRAGIVGEDGETHAGAFDYSYMRCIPNMLIMAPADENECRQMLTT 463
                                                                                                                                                                                                                                        VKYHAVAN-----LPKESAAQMPSEKEPKPAAKPTYTQVFGKWLCDRAAADSRLVAIT
                                                                                                                                                                                                                                                                                                                                                                                                    VGALPKYLASNVVRDMHGLLSTVKAQTGKVLDKIPGAMEPAQKVEHKIKTLAEEAEHAKQ 244
                                                                                                                                                       PAMREGSGLVEFEQRFPDRYFDVGIAEQHAVTFAGGLACEGMKPVVAIYSTFLQRAYDQL
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B, strain MC58
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A;Cross-references: GB:AP000398;
A;Experimental source: strain APS
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R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa,
Nature 407, 81-86, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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A;Status: preliminary
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NIGLPDRFVEQGSREELLSLVGLDSKGI
                                        VGELLMD-MURIPIGKSLIKRRGKKIAILNFGILLHNAYCAAEKLDATLUDMRFVKPLDK
                                                                            PGAAIDPTLTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQ
                                                                                                             GIVGNDGQTHQGVFDLAYLRCIPGIVIMTPSNENECROMLYTGYMHNKGPSVVRYPKGYG
                                                                                                                                            GLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFOHH-GPASVRYPRGKG
                                                                                                                                                                         QYFDVAIAEQHAVTFAAGLAISGYKPVVSIYSTFFQRAYDQLIHDIALQKLSVLFAVDRA
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                                                                                                                                                                                                                                                          FEELGFNYFGPIDGHDVEMLVSTLENLKOLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVP 301
                                                                                                                                                                                                                                                                                                                                                                    NVGALNKHL-KILRSVQNTQKNRKKIRLLNKKLFFK-----DKRIQNH---SISFNSI
                                                                                                                                                                                                                                                                                                                                                                                                   PVGAMNNYLTKVLSS-----KFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YPLIKNIHTPADIRALSKDQIQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVF 66
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                                                                                                                                                                                                                                                                                                       FSNLGCKYLGPFDGHNIFSIINTLKKIKNKKGTYLLHLVTKKGKGYLPABLNPIKWHTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           51.8%; Score 1667; DB 2; ilarity 52.8%; Pred. No. 4.4e-109; Conservative il8; Mismatches 146;

    Buchnera sp.

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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: The complete genome of the hyperthermophilic bacterium A; Reference number: A70300; MUID:98196666; PMID:9537320
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; nucleic acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species: Aquifex aeolicus;Date: 08-May-1998 #text_change 24-Sep-1999;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 24-Sep-1999;Accession: A70376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;Molecule type: DNA
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                                                                                                V---PTEGFKKIEIGTWEELLEGEDCVILAVGYPVYQALRAAEKLYKEGIRVGVVNARFV
                                                                                                                                                                                                                                                                                                         YEDVATABQHAVTLAAGQACQGAKEVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAG
                                                                                                                                                                                                                                                                                                                                                       ELGFNYIGPIDGHDIKALEDTLNNVKDIKGPVLLHVYTKKGKGYKPABENPVKWHGVAPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPPEDVIVMDIGHQGYPMKILTDRKEQFFTLRQYKGISGFLRRESIYDAFGAGHSSTSI 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESBYDAFGVGHSSTSI
      SREELLSLVGLDSKGI 61:
                                                              KPPDQALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVIMPVCNIGLPDRFVEQG
                                                                                                                             AAIDPT--LTALEIGKAEVRHHGSRIAILAWGSMVTPAVEAGKQL-----GATVVNMRFV
                                                                                                                                                              LVGDDGPTHHGVFDLSYLRCVPNMVVCAPKDEQELRDLLYTGIYSGKPFALRYPRGAAYG
                                                                                                                                                                                          LVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQHHGPASVRYPRGKGPG
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                                   KPMDEKMLRDLANRYDTF1TVEDNTVVGGFGSGVLEFFAREGIMKRVINLGVPDRF1EHG
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Pred. No. 8.6e-106;
5; Mismatches 174;
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A;Status: preliminary
A;Status: preliminary
A;Residues: 1-643 <KUR>
A;Residues: 1-643 <KUR>
A;Cross-references: GB:AB008917; PIDN:AAL52679.1; PID:g17983505; GSPDB:GN00190
A;Experimental source: strain 16M
C;Genetics:
A;Gene: BMEIL498
A;Map position: I
C;Superfamily: hypothetical protein C2814
C;Keywords: carbon-oxygen lyase; hydro-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Brucella
C;Date: 01-Feb-2002
C;Accession: AD3439
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A;Title: The genome sequence of the facultative intracellular pathogen Brucella melitens A;Reference number: AD3252; PMID:11756688
A;Accession: AD3439
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Best Local
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REELLSLYGLDSKGILATI 615
                                                                                        QALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQXVL---MPVCNIGLPDRFVEQGS
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51.4%; Pred. No. 9.66
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(G97505)
1-deoxyxylulose-5-phosphate synthase [imported] - Caulobacter crescentus
1-deoxyxylulose-5-phosphate synthase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C;Accession: C87505
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Bisen, J.; Heidelberg, J.
B.; Laub, W.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession. C87505
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A;Residues: 1-640 <STO>
A;Cross-references: GB:AE005673; NID:gl3423547; PIDN:AAK24039.1; GSPDB:GN00148
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C; Superfamily:
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QDQDKPDAMYAQAGLDAEGIL
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                                      VEQGSREELLSLVGLDSKGIL 612
                                                                            AKPLDLDLLLRLAREHBAIITVEEGSM-GGFGAFVLQALAQHGALDRGLKIRTLCLPDVF
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97; Mismatches 196; Indels
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Search completed: January 29, 2004, 15:55:29 Job time : 20.2424 secs

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Result
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   SwissProt_41:*
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OBz83 salmonella
OBzrd1 salmonella
OBxx95 ralstonia s
P77488 escherichia
OBfkb9 escherichia
OBrkb9 escherichia
OBp815 xanthomonas
                                    95/89197
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Q8egr9 shewanella
Q8zc45 yersinia pe
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Q9ktl3 vibrio chol
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5 xylella fas
5 xylella fas
5 haemophilus
5 haemophilus
7 wiggleswort
3 neisseria m
                                    6 buchnera ap

1 buchnera ap

6 aquifex aeo

2 brucella me

2 brucella me

2 brucella me

3 rhizobium 1

5 caulobacter

5 thermoanaer

7 agrobacteri

9 agrobacteri

1 rhizobium

1 rhizobium

1 bacillus ha
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5 ralstonia s
8 escherichia
9 escherichia
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xanthomonas
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629	609	619	633	719	632	641	717	594	636	635	636
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DXS_DEIRA	DXS_LISMO	DXS_CLOAB	DXS BACSU	DXS CAPAN	DXS_LISIN	DXS RHOCA	DXS ARATH	DXS ORYSA	DXS_SYNP7	DXS ANASP	DXS_SYNLE
	Q8y7c1	Q97hd5	P54523	078328	Q92bz0		Q38854			Q8yz80	Q9r6s7
deinococcus	listeria mo	clostridium	bacillus su	capsicum an	listeria in	rhodobacter	arabidopsis	oryza sativ	symechococc	anabaena sp	synechococc

ALIGNMENTS

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EMBL; AE016798; AAO08845.1; HAMAP; MF.00315; -; 1. InterPro; IPR005477; Dxs. InterPro; IPR005477; Dxs. InterPro; IPR005475; Transketolase_C. InterPro; IPR005475; Transketolase_CR. InterPro; IPR005474; Transketolase_N. Pfam; PF02799; transketolase_C; 1. Pfam; PF02799; transket pyr; 1. TIGR0204; dxs; 1. PROSITE; PS00801; TRANSKETOLASE_1; 1. PROSITE; PS00802; TRANSKETOLASE_1; 1. PROSITE; PS00802; TRANSKETOLASE_1; 1. Transferase; Flavoprotein; Thiamine pyrophosphate; Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome. SEQUENCE 621 AA; 67959 MW; 69DABA88B2ZBB04B CRC64;	42, Created) 42, Last sequen 42, Last sequen 42, Last sequen 88 5-phosphate synthas 88 5-phosphate synthas 88 5-phosphate synthas 8	LT 1 VIBVU DXS VIBVU STANDARD; PRT; 621 AA.

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SEQUENCE FROM N.A.

STRAIN-EI TOR N16961 / Serotype O1;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

podson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayyam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Dragoi I., Sellers P

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
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Matches
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Pfam; PF02780; transketColase_C; 1.
Pfam; PF02780; transketColase_C; 1.
TIGRFAMs; TIGRO0204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
Transferase; Flavoprotein; Thiamine pyrophosphate; Isoprene biosynthesis; Thiamine biosynthesis; Comp SEQUENCE 626 AA; 68346 MW; 5E83BF99EE8C51C9 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMMI cultration the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005475; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
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Fraser C.M.;
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Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: Homodimer (By similarity).
SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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PNRYFDVAIAEQHAVILAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALD
                                          VPKFDPSHHSLPKSS-NTKPTFSKIFGDFLCDMAAQDPKLMAITPAMREGSGMVRPSKEY
                                                                                                                                                                             NDMSISPPYGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWBELARKTBEHVKGMIVPG
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K MEDLINE-20437337; PubMed=10984043;

K MEDLINE-20437337; PubMed=10984043;

K MEDLINE-20437337; PubMed=10984043;

K Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

K Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

K Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

K Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

K Garber S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

K Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

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K Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

K Smith K.A., Spencer D.H., Wo
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)9GU7;
16-OCT-2001 (Rel. 40, Created, Incomplete update, 16-OCT-2001 (Rel. 40, Last sequence update, 15-SEP-2003 (Rel. 42, Last annotation update) 15-Aeoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Tools for discovery of inhibitors of the 1-deoxy-D-xylulose 5-phosphate (DXP) synthase and DXP reductoisomerase: an approacenzymes from the pathogenic bacterium pseudomonas aeruginosa."; FEMS Microbiol. Lett. 190:329-333(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND CHARACTERIZATION MEDLINE=20487113; Pubmed=11034300;
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Bacteria; Proteobacteria; Gammaproteobacteria;
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s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restriby non-profit institutions as long as its content if the statement is not removed. Usage by and
                                                                                                                                 SUBUNIT: Homodimer (By similarity). SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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                                                                                                                                           LDAAGIEKAVRQ
                              STANDARD;
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IRMAP, MF_00315; 7; 1.

InterPro; IPR005477; Dxs.

InterPro; IPR005476; Transketolase_C.

InterPro; IPR005474; Transketolase_CR.

InterPro; IPR005474; Transketolase_CR.

InterPro; IPR005474; Transketolase_C.

Pfam; PF02779; transket_Dyr; 1.

Pfam; PF02780; transket_Dyr; 1.

ITGRPAMS; TIGR00204; dxs; 1.

ITGRPAMS; TIGR00204; dxs; 1.

PROSITE; PS00801; TRANSKETOLASE_1; FALSE_NEG.
PROSITE; PS00802; TRANSKETOLASE_2; FALSE_NEG.

PROSITE; PS00802; TRANSKETOLASE_1; Complet is propense biosynthesis; Complet is propense biosynthesis; Complet SEQUENCE 627 AA; 68049 MM; EBEP04296FF6D57D CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF282878; AAF97240.1; -. EMBL; AE004821; AAG07431.1; -.
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an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                           PDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMITTGFQHHGPASVRYPRGKGPGAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPTK 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELIGF 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVFN
                                                                                LARTHDVFVTVBENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLSLVG
                                                                                                                                                                                                                                   BDGETHAGSFDISYLRCIPGMLVMTPSDEDELRKLLTTGYLFDGEAAVRYERGSGENHEI
                                                                                                                                                                                                                                                                                                                                   VAIAEQHAVTLAAGMACEGMKPVVAIYSTFLQRAYDQLIHDVAVQHLDVLFAIDRAGLVG
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                                                                                                                                        DPDLQPVEIGKGVVRRRGGRVALLVFGVQLAEAMKVABSLDATVVDMRFVKPLDEALVRE
                                                <u>LAGSHELL VTI EENAVMGGAGSAVGEPLASEGLEVPLLQLGLPDYYVEHAKPSEMLAECG</u>
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Pred. No. 3.96
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BBEF04296FF6D57D CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .9e-138;
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Matches 383
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Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
Deboy R. T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
"Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis.",
                                                                                                                                                                                            PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00802; TRANSKETOLASE_2; 1.
Transferase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete
SEQUENCE 622 AA; 68083 MM; BE681C01BEA5EFB4 CRC64;
                                                                                                                                                                                                                                                                             Pfam; PF02780; transketolase_C;
Pfam; PF02779; transket_pyr; 1.
TIGRFAMs; TIGRO0204; dxs; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heidelberg J.F., Pauls
Read T.D., Eisen J.A.,
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
deoxyxylulose-5-phosphate synthase) (DXP synthase) (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (S or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alteromonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                   [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: Catalyzes the acyloin condensation reaction betwee atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity). CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate deoxy-D-xylulose 5-phosphate + CO(2). COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY: Biosynthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Biotechnol. 20:1118-1123(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                   AE015598; AAN54586.1; -. S01525; -.
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                            VENTPVDQLVWDVGHQAYPHKILTGRKERMFTIRTLGGVSAFPARDESEYDAFGVGHSST
                                                                                   TDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVBLTVALHY
VYNTPFDRLIMDVGHQAYPHKILTGRRDRMHTIRQKNGLHPFPMREESEYDTFSVGHSGT
                                                                                                                                                                                                                                                                                                                            IPR005477; Dxs.
IPR005476; Transketolase_C.
IPR005475; Transketolase_CR.
IPR005474; Transketolase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homodimer (By similarity).
TY: Belongs to the transketolase family. DXPS subfamily.
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                                                                                                                                               62.0%;
                                                                                                                                 105;
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                                                                                                                                               Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ., Nelson K.E., Gaidos E.J., Nelson dri R., Ward N., Methe B., Clayton
                                                                                                                                 Mismatches
                                                                                                                                               2042;
No. 3
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thiamine and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
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                                                                                                                                               DB 1;
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DIQLDAEGMLAQINAYLA
                             LVGLDSKGILATIEQFCA
                                                                                VLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGSREELLS
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                                                            VKEMAQTHDVLVTVEENAIMGGAGSGVLELLQQLKMPKPVLQIGLPDEFIKHGSPDEVIH
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YERPE
DXS YERI
Q8ZC45;
                                                                                                                                                            STRAIN=CO-92 / Biovar Orientalis;

MEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Paker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague

Nature 413:523-527(2001).
SEQUENCE FROM N.A.

STRAIR=KIM5 / Biovar Mediaevalis;

STRAIR=KIM5 / Biovar Mediaevalis;

MEDLINE=22137863; PubMed=12142430;

Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C., Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.

Straley S.C., McDonough K.A., Nilles M.L., Matson J.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2
deoxyxylulose-5-phosphate synthase) (DXP synt
DXS OR YP03177 OR Y100B.
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM
STRAIN=CO-92
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Yersinia pestis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DXP synthase)
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"Genome sequence of Yersinia pestis KIM.";

J. Bacteriol. 184:4601-4611(2002).

-1- FUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (Party) (By similarity).

-1- CATALYTIC ACTIVITY: Byruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2).

-2- CATALTIC ACTIVITY: Byruvate + CO(2).

-3- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By similarity).

-3- Similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HAMAP: MF_00315; -; 1.
InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005475; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AJ414155; CAC92412.1; -. EMBL; AE013704; AAM84589.1; -.
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PROSITE; PS00802; TRANSKETOLASE 2; 1.

Transferase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Comp
SEQUENCE 619 AA; 67673 MW; B528BE47650AA296 CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02779; transket pyr; 1.
Pfam; PF02780; transketolase_C; 1.
TIGRFAMs; TIGR00204; dxs; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMEL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: Belongs to the transketolase family.
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                                                                                         KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRYFDV
                                                                                                                                                                 FNYFGPIDGHDVEMLVSTLENLKDLTGBVFLHVVTKKGKGYAPAEKDPLAYHGVPAFDPT
                                                                                                                                                                                                          PVGAMMYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELG
                                                                                                                                                                                                                                                                                                               SAALCMAIASQLRGEDKKKKVAIIGDGSITGGWAYEAMNHAGDVNANLLVILNDNDWSISP 186
                                                                                                                                                                                                                                                                                                                                                     NTPFDHLIWDVGHQAYPHKILTGRRDRISTIRQKDGLHPFPWRGESBYDVLSVGHSSTSI
                                                                                                                                                                                                                                                                                                                                                                         NTPVDQLVWDVGHQAYPHKILTGRXERMFTIRTLGGVSAFPARDESEYDAFGVGHSSTSI 126
                                                                                                                                                                                                                                                                                                                                                                                                                      PTLALAENPEELRMLPKESLPKLCDELRQYLLTCVSRSGHPASGLGVVELTVALHYVY
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AIAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALDRAGLVGP 426
                                                                   SGTLPK-SQSSLPTYSKIFGEWLCETAAKDSKLMAVTPAMREGSGMVRFSREYPQQYFDV
                                                                                                                                      FNY I GPVDGHDVHTLTQTLKNMRDLKS PQLLHIMTKKGKGYAPABKDPI GWHAVPKFDPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.7%; Score 2015; DB 1; 61.6%; Pred. No. 2.7e-134; tive 95; Mismatches 139;
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STRAIN-Ty2 / ATCC 700931;

MEDLINE=22531367; PubMed=12644504;

MEDLINE=22531367; PubMedt G. III, Mayhew G.F., Rose D.J.,

Beng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi strains
and CT18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21534947; PubMed=11677608;
Parkhill J., Dougan G., James R.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
This SWISS-PROT entry is copyright. It is produced through a collabora between the Swiss Institute of Bioinformatics and the EMBL outstati the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         deoxyxylulose-5-phosphate synthase)
DXS OR STY0461 OR T2441.
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15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
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Enterobacteriaceae; Salmonella.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003
                                                                                     step.
SUBUNIT: Homodimer (By similarity).
SIMINARITY: Belongs to the transketolase family. DXPS subfamily.
                                                                                                                                             PATHWAY: Biosynthetic
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                                                                                                                                                          similarity).
PATHWAY: Non
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SOURCE SERVICE RESULT 7
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Piam; P702780; transketolase C; 1.
TIGRPAMs; TIGR00204; dxs; 1.
PROSITE; P$00801; TRANSKETOLASE 1; 1.
PROSITE; P$00802; TRANSKETOLASE 2; 1.
Transferase; Plavoprotein; Thiamine pyrophosphate;
Transferase; Plavoprotein; Thiamine biosynthesis; Complete proteome.
INIT_MET 0

BY SIMILARITY.
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HAMAP; MF 00315; -; 1.

InterPro; IPR005477; Dxs.

InterPro; IPR005476; Transketolase C.

InterPro; IPR005475; Transketolase CR.

InterPro; IPR005474; Transketolase_N.
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                                                                                                                                                                                                            LARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMFVCNIGLFDRFVEQGSREELLSLVG
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                                                                                                                                                                             MAAQHDALVTLEENAIMGGAGSGVNEVLMAHRKPVPVLNIGLPDFFIPQGTQEEARAELG
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                                                                                                            LDAAGIEAKIKAWLA
                                                                                                                                         LDSKGILATIBQFCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      619 AA;
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                      STANDARD,
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Pred. No. 2.9
                        PRT;
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Query Match
Best Local S
Matches 375
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InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005475; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
Pfam; PF02779; transket pyr; 1.
Pfam; PF02789; transketolase_C; 1.
Pfam; PF02780; transketolase_C; 1.
TICRPPMS; TICR00204, dxs; 1.
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Nature 413:852-856(2001).

PUNCTION: Catalyzes the acyloin condensation reaction between atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yi 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).

PORTALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = deoxy-D-xylulose 5-phosphate + CO(2).

Geoxy-D-xylulose 5-phosphate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-LT2 / SGSC1442 / ATCC 700720;
MEDLINE-21534948; PubMed-11677609;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P. Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman I. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan B., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.
deoxyxylulose-5-phosphate synthase) (DXP synthase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              deoxyxylulose-5-phosphate pxs or STM0422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Eventhe European Bioinformatics Translation                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
Enterobacteriaceae; Salmon
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PROSITE; PS00802; TRANSKETOLASE 2; 1.
Transferase; Plavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome.
INIT_MET 0 0 BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBUNIT: Homodimer (By similarity).
SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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SAALGWAIASQLRGEDKKWYAIIGDGSITGGWAYEAMNHAGDVNANLLVILNDNDWSISP
                                                        NTPFDQL1WDVGHQAYPHKILTGRRDK1GT1RQXGGLHPFPWRGBSEYDVLSVGHSSTSI
                                                                                       NTPVDQLVMDVGHQAYDHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSSTSI
                                                                                                                                                                        YPTLALVDSTQELRLLPKESLPKLCDELRRYLLDSVSRSSGHPASGLGTVELTVALHYVY
                                                                                                                                                                                                          YPLIKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVELTVALHYVF
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                                                                                                                                                                                                                                                                                           Score 2013.5;
Pred. No. 3.4e.
06; Mismatches
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pyridoxol;
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                                                       Salanoubat M., Genin S., Artiguenave P., Gouzy J., Mangenot S.,
Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Demange N.,
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
Siguier P., Thebault P., Whalen M., Wincker P., Levy M.,
Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearum.";
Nature 415:497-502(2002).

-i- FUNCTION: Catalyzes the acyloin condensation reaction between C
atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield
1-deoxy-D-xylulose-5-phosphate (DXP) By similarity).
-i- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-
deoxy-D-xylulose-5-phosphate + CO(2).
                                                                                                                                                                                                                                                                         DXS_RALSO STANDARD; PRT; 636 AA.

QBXX95;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-Dxylulose 5-phosphate synthase (BC 2.2.1.7)
deoxyxy-ulose-5-phosphate synthase) (DXP synthase)
DXS_OR_RSC2221 OR_RS01378.
                                                                                                                                                                                                                                            Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
Burkholderiaceae; Ralstonia.
                                                                                                                                                                                           STRAIN=GMI1000;
MEDLINE=21681879; PubMed=11823852;
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SUBUNIT:
                                                 COFACTOR: Binds 1
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                Nonmevalonate terpenoid Biosynthetic pathway to
Homodimer (By
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                                                thiamine pyrophosphate
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similarity)
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thiamine and
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                  pathway; f:
pyridoxol;
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  RESULSINGUSKGILATISQ
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HAMAP, MF_00315; -; 1.

InterPro; IPR001017; Dehydrogenase_E1.

InterPro; IPR005476; Dxs.

InterPro; IPR005476; Transketolase_C.

InterPro; IPR005476; Transketolase_CR.

InterPro; IPR005476; Transketolase_CR.

InterPro; IPR005474; Transketolase_CR.

InterPro; IPR005474; Transketolase_CR.

Ifam; PP02779; transketolase_C; 1.

Pfam; PP02780; transketolase_C; 1.

IGRPAMs; TIGR00204; dxs; 1.

PROSITE; PS00801; TRANSKETOLASE_1; 1.

PROSITE; PS00802; TRANSKETOLASE_2; 1.

PROSITE; PS00802; TRANSKETOLASE_2; 1.

Igoprene biosynthesis; Thiamine biosynthesis; Complete the prosection of the prosection of the property of the prosection of the prosection of the prosection of the property of the prosection of the prosection of the prosection of the property of the prosection of the property of the prosection of the property of the pro
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PLDAACVLEMARTHDYVVTVERGCVMGGACSACLEALAAAGVATPVLQLGLPDRFVDHGD
                                     PFDQALVLELARTHDVFVTVEENVIAGGAGSAINTFLQAQKVLMPVCNIGLPDRFVEQGS
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; Pred. No. 7.9e-134;
92; Mismatches 134;
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RESULT >
DXS_ECOLI
TYT488;
P77488;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MBDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F. Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J., Mau B., Shao Y.;
                                                                                                                                        J. Bacteriol. 182:891-897(2000).
-!- FUNCTION: Catalyzes the acyloin condensation reactoms 2 and 3 of pyruvate and glyceraldehyde 3-F1-deoxy-D-xylulose-5-phosphate (DXP)
-!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde deoxy-D-xylulose 5-phosphate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roberts D., Allen E., Araujo R., Aparicio A., Chung E., Davis Duncan M., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi Lew H., Lin D., Namath A., Oefner P., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D-1-deoxyxylulose 5-phosphate, a common precursor
thiamin, and pyridoxol biosynthesis.";
Proc. Natl. Acad. Sci. U.S.A. 95:2105-2110(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=98058734; PubMed=9371765; Sprenger G.A., Schorken U., Wiegert T., Grolle S., de Sprenger G.A., Schorken U., Wieger-Meyer S., Sahm H.; Taylor S.V., Begley T.P., Bringer-Meyer S. Sahm H.; "Identification of a thiamin-dependent synthase in Es required for the formation of the 1-deoxy-D-xy/lulose precursor to isogrenoids, thiamin, and pyridoxol."; proc. Natl. Acad. Sci. U.S.A. 94:12857-12862(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The complete genome sequence of Escherichia coli K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                                                                                                                                                                                      Kuzuyama T., Takagi M., Takahashi S., Seto H., Tokahashi S., Seto H., Tokahashi S., Seto H., Sela H., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-6, AND CHARACTERIZATION.
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                                                                                                                                                                                                                                                                                                biosynthesis.";
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                                             PATHWAY:
                                                                                                                        COFACTOR: Binds 1 thiamine pyrophosphate
SUBUNIT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RcoGene; EG13612; dxs...
HAMAP; MF 00315; -; 1.
InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005475; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
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EMBL; U82664; AAB40
PIR; D64771; D64771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- MISCELLANEOUS: Optimal temperature is 42-44 degrees Celsius and optimal pH is 7.5-8.0.
-!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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PROSITE; PS00802; TRANSKETOLASE 2; 1.

Transferase; Flavoprotein; Thiamine pyrophosphate;

Isoprene biosynthesis; Thiamine biosynthesis; Manganese; Magnesium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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PF02780; transketolase_C; 1.
AMs; TIGR00204; dxs; 1.
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                          DPTLTALBIGKAEVRHHGSRIAILAWGSWVTPAVEAGKQLGATVVNMRFVKPFDQALVLE
                                                                      DGPTHAGAEDYSYMRCIPNMLIMAPADENECROMLTTGFQHH-GPASVRYPRGKGPGAAI
                                                                                                              AIAEOHAVTLAAGOACOGAKPVVAIYSTFLORGYDQLIHDVALQNLDMLFALDRAGLVGP
                                                                                                                                                                                                    KDFLPKAAPSPHPTYTEVFGRWLCDMAAQDERLLGITPAMREGSGLVEFSQKFPNRYFDV
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                                                         DGQTHQGAFDLSYLRC1PEMVIMTPSDENECRQMLYTGYHYNDGPSAVRYPRGNAVGVEL
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114; Mismatches
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Pred. No. 2.8
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A Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

A Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

A Mashew G.F., Rose D.J., Zhou S.-R., Boutin A., Hackett J., Stroud D.,

A Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

A Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome sequence of uropathogenic Escherichia coli.";

Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

L. Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

- PUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield complete acyloise-5-phosphate (DXP) (By similarity).

- 1- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-

C decoy-D-xylulose-5-phosphate + CO(2).

- 1- COPACTOR: Binds 1 thiamine pyrophosphate per subunit (By
Query Match
Best Local
                                                                                            EMBL; AE016756; AAN79009.1; -.

HAMAP; MF 00315; -; 1.

InterPro; IPR005477; Dxs.

InterPro; IPR005475; Transketolase_C.

InterPro; IPR005475; Transketolase_CR.

InterPro; IPR005474; Transketolase_CR.

InterPro; IPR005474; Transketolase_C.

Pfam; PF02780; transketolase_C; 1.

Pfam; PF02780; transket_pyr; 1.

Pfam; PF0279; transket_pyr; 1.

TIGRPAMS; TIGR00204; dxs; 1.

TIGRPAMS; TIGR00204; dxs
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
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SIMILARITY: Belongs to the transketolase family.
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         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-decoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
decxyxylulose-5-phosphate synthase) (DXP synthase) (DXS OX 20523 OR ECS0474.
                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                      NCBI_TaxID=83334;
                                                                                                                                                      Escherichia coli 0157:H7.
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RC STRAIN=0157:H7 / RND 0509952;

RM MBDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Han C.-G., Shiba T., Hattori M., Shinagawa H.;

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;

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RA Kuhara S., Shib
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PROSITE; PS00802; TRANSKETOLASE_2; 1.
Transferase; Flavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome.
INIT_MET 0 0 BY SIMILARITY.
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InterPro; IPR005477; Dxs.

InterPro; IPR005476; Transketolase_C.

InterPro; IPR005475; Transketolase_CR.

InterPro; IPR005474; Transketolase_N.

Pfam; PF02779; transket_pyr; 1.

Pfam; PF02780; transketolase_C; 1.
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F85538; F85538.
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                                                                                                   PVGAMNNYLTKVLSSKFYSSVREESKKALAKMPSVWELARKTEEHVKGMIVPGTLFEELG
                                                                                                                                                                     SAALGWAIASQLRGEDKKWVAIIGDGSITGGWAYEAMNHAGDVNANLLVILNDNDMSISP
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                                                                                                                                                                                                                                                                NTPFDQLIWDVGHQAYPHKILTGRRDKIGTIRQKGGLHPFPWRGESEYDVLSVGHSSTSI
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59.8%;
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Pred. No. 6.3e
15; Mismatches
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RC STRAIN=ATCC 33913 / NCPPB 528;

RC MEDDINE=22022145; PubMed=12024217;

RX MEDDINE=22022145; PubMed=12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Canargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Cannavan P., Cardozo J., Chambergo F., Ciapina L.P.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,

RA Fornighteri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Fornighteri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Percira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RT Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RT Thost specificities ",

RT host specificities ",
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XANCP
                                                                                             Nature 417:459-463(2002).

-i-FUNCTION: Catalyzes the acyloin condensation reaction between atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to y.

1-deoxy-D-xylulose-5-phosphate (NXP) (By similarity).

-i- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = deoxy-D-xylulose 5-phosphate + CO(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   deoxyxylulose-5-phosphate synthase)
DXS OR XCC2434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J8P815;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
1-deoxy-D-xylulose 5-phosphate synthase) (DXP synthase) (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=340;
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                                                                                                                                                                                                               host specificities.
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                Nonmevalonate terpenoid biosynthesis Biosynthetic pathway to thiamine and
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SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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                                                                                                                                                                 GPGAAIDPTLTALEIGKAEVRHHGSRIAILAWGSWVTPAVEAGKQLGATVVNMRFVKPFD
                                                                                                                                                                                                                                RAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECROMLTTGFQHHGPASVRYPRGK 479
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                                                                                                QALVLELARTHDVFVTVEENVIAGGAGSAINTFIQAQKVLMPVCNIGLPDRFVEQGSREB
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LLAEAGIDQAGIRAAV
                               LLSLVGLDSKGILATI 615
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RX KEDLINE-2002/145; Pubmedel120/4217;
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Quaggio R.B., Containho L.L., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M., Moreira J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Gruber A.,
RA Formighieri B.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Xishi L.T., Leite R.P., Lemos B.G.M., Lemos M.V.F.,
RA Katsuyama A.M., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meddanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Martins E.C., Takkta M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Spinola L.A.F., Takkta M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Spinola L.A.F., Takkta M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Stubal J.C., Kitajima J.P.,
RA Stu
R HAMAP; MS 00315; -; 1.

R HAMAP; MS 00315; -; 1.

R InterPro; IPR005477; Dxs.

R InterPro; IPR005476; Transketolase_C.

R InterPro; IPR005475; Transketolase_CR.

R InterPro; IPR005474; Transketolase_CR.

R InterPro; IPR005474; Transketolase_C.

R Pfam; PF02779; transket pyr; 1.

R Pfam; PF02780; transket pyr; 1.

R Pfam; PF02780; transketolase_C; 1.

R Pfam; PF02780; transketolase_C; 1.

R Pfam; PF0279; transketolase_C; 1.

R Pfam; PF0279; Transketolase_C; 1.

R Pfam; PF0279; Transketolase_C; 1.

R Pf03ITE; PS00801; TRANSKETOLASE 1; 1.

R PROSITE; PS00802; TRANSKETOLASE 1; 1.

R PROSITE; PS00802; TRANSKETOLASE 1; Complete prophosphate;

W Transferase; Plavoprotein; Thiamine bjosynthesis; Complete prophosphate;

O SEQUENCE 638 AA; 68479 MW; 3D739EE912C17CF7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/anor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8PJG7;
28-FEB-2003
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DXS OR XAC2565.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: Homodimer (By similarity).
-!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
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06 / ATCC 13902 / XV 101;
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thiamine and pyridoxol;
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PASMU
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                                                                                                                                                                                                                    SEQUENCE
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Pasteurellaceae; Pasteure
                                                                                                                                                                                                                                                                                                                                       Pasteurella multocida.
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61.4%; Pred. No. 2.8e
tive 91; Mismatches
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Matches 369
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R HAMAP; MF 00315; -; 1

R InterPro; IPR005477; Dxs.

InterPro; IPR005475; Transketclase C.

InterPro; IPR005475; Transketclase CR.

InterPro; IPR005474; Transketclase CR.

Pfam; PF02779; transket Dyr; 1

Pfam; PF02779; transket Dyr; 1.

Pfam; PF02780; transket Dyr; 1.

Pfam; PF02780; transket Dase C; 1.

PFGSITE; PS00801; TRANSKETOLASE 1; 1.

PROSITE; PS00802; TRANSKETOLASE 2; 1.

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CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate
deoxy-D-xylulose 5-phosphate + CO(2).
COPACTOR: Binds 1 thiamine pyrophosphate per subunit (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBUNIT: Homodimer (By similarity). SIMILARITY: Belongs to the transketolase
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                                                 LTP-LTMLALGKSNLIREGEKIAILNFGTLLPTAINVAEKLNATVIDMREVKPIDVERIH
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                                                                                                IDPTLTALEIGKAEVRHIGSRIAILAWGSMVTPAVEAGKQLGATVVNMRFVKPFDQALVL
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GLDSKGILATIEQF 618

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RX MEDLINE=20365717; PubMed=10910347;
RX MEDLINE=20365717; PubMed=10910347;
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bove J.M., Briones M.R.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Colambo C.D., Costa F.E., Costa M.C.R., Costa-Neto C.M.,
RA Glarier M., Golombo C., Costa F.E., Costa M.C., Franco D.M., Carrer H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Fraga J.S., Franca S.C., Franco M.C., Erohme M., Furlan L.R.,
RA Krieger J.E., Kuramae E.E., Laigret F. Lambais M.R., Leite L.C.C.,
RA Marques M.V., Martins B.A.L., Martins E.M.F., Machado J.A.,
RA Marques M.V., Martins B.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins B.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manda C.F.M., Miracca B.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Menok C.F.M., Miracca B.C., Niyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Menok C.F.M., Obiveira R.C., Palmieri D.A., Paris A.,
Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA de Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsihako M.H.,
RA de Solva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsihako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Vallada H., Jan 3 to five Palart pathogen Xylella fastidiosa.",
RT The genome sequence of the plant pathogen Sylella fastidiosa.",
RT Function: Catalyzes the acyloin condensation reaction between C.
C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. - 1 to C. 
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Xanthomonadaceae; Xylella.
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ween the Swiss Institute of Bioinformatics and the EMBS outstations on
European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
                                                                                                               SUBUNIT: Hom
                                                                                                                                                                                                                                                       FUNCTION: Catalyzes the acyloin condensation reaction between C atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity). CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-deoxy-D-xylulose 5-phosphate + CO(2). COPACTOR: Binds 1 thiamine pyrophosphate per subunit (By
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                                                                                                               Homodimer (By similarity).
TY: Belongs to the transketolase family. DXPS subfamily.
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InterPro; IPR005477; Dxs.

InterPro; IPR005475; Transketolase C
InterPro; IPR005475; Transketolase C
InterPro; IPR005474; Transketolase C
InterPro; IPR005474; Transketolase N
Pfam; PF02780; transketolase C; 1.

Pfam; PF02780; transketolase C; 1.

TIGRPAMS; TIGR00204; dxs; 1.
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PROSITE; PS00802; TRANSKETOLASE 2; FRALE NEG.
Transferase; Plavoprotein; Thiamine pyrophosphate;
Isoprene biosynthesis; Thiamine biosynthesis; Complete
SEQUENCE 635 AA; 68408 MW; 18567FA8CDDDDBZE CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                               TSISAALGMAIASQLRGEDKKKWALIGDGSITGGMAYEAMNHAGDVN--ANLLVILNDND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YVFNTPVDQLVWDVGHQAYPHKILTGRKERMPTIRTLGGVSAFPARDESEYDAFGVGHSS
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                                                                                                                                                                                                                                                                                                                                                                             MSISEAVGGLTKMLGRATGSKALAAIREGGKRIFGDKKTNATARFLRRWEEHWKGMFVPS
                                                                                                                                                                                                                                                                                                                                                                                                      MSISPPVGAMNNYLTKVLSSKFYSSVREESKKALA--KMPSVWELARKTEEHVKGMIVPG 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YLYCTPIDHLVWDVGHQTYPHKILTGRRDKISTVKHQGGLAPPPKREESIYDTFGVGHSS
                                                                                                     GPGAAIDPTLTALEIGKAEVRHHGSRIAILAMGSMVTPAVEAGKQLGATVVNMRFVKPPD
                                                                                                                                                                                  RAGLVGPDGPTHAGAFDYSYMRCIPNMLIMAPADENECRQMLTTGFQHHGPASVRYPRGK 479
                                                                                                                                                                                                                             PNRYFDVALAEQHAVTLAAGQACQGAKPVVAIYSTFLQRGYDQLIHDVALQNLDMLFALD 419
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                                                                                                                                                                                                                                                                                                                                                    TLFEELGFNYFGPIDGHDVEMLVSTLENLKDLTGPVFLHVVTKKGKGYAPAEKDPLAYHG 299
||: |:|: |: |: |: |: |
                                                   RTLLLELARTHEGFYTIEDNYVAGGAGSGVAELLNAEGIVLPIVHLGLPDAFQQHASRED
                                                                   PQRYFDVAIABQHAITLAAGMATQGAKPVVAIYSTFLQRGYDQLVHDVALQKLDVLFAVD
                           LLSLVGLDSKGILATI 615
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59.3%;
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Transketolase_CR.
Transketolase_N.
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Search completed: January 29, 2004, 15:50:38 Job time: 12.6752 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
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Gapop 10.0 , Gapext 0.5
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1 MKLTTDYPLLKNIHTPADIR.....LSLVGLDSKGILATIEQFCA 620
sp_mhc:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_virus:*
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sp_vricbrate:*
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sp_bacteriap:*
sp_archeap:*
                                                                                                                                                                                     sp_human:*
sp_invertebrate:*
sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

3 1999.5 62.2 620 16 QBFKB9 4 1795 55.8 62.6 16 QBG29.7 5 1592.5 49.5 643 16 QBG29.2 6 1498.5 46.6 644 16 QBKFI9 7 1482.5 46.1 716 10 QBKFI9 9 1444.5 44.9 711 10 QBL692 10 1440.5 44.8 715 10 QBL692	Query Match Len 65.7 63.5
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O9wxf0 deinococcus	Q9fev6 nicotiana t	Q8g585 bifidobacte		77		~1	arabidops			Q8r606 fusobacteri	Lactococcu	Q9cf08 lactococcus			Q9lfl9 arabidopsis	Q9sngl oryza sativ	Q8cjp7 streptomyce	7		Q8fpi2 corynebacte					4.	Q9xh50 lycopersico	Q9fv39 tagetes ere	O64904 mentha pipe	

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ZAMNHAGDY	LRGEDKKM	61 VALHYVYNTPEDQLIMDVGHQAYPHKILTGRREQMPTIRQKGGLHPFPMREBSEYDTLSV 120		1 MTLDISKYPTLALAETEDELRLLPKETLPTLCDELRTYLLNSVSQSGHLASGLGTVELT 60	VALSKDQLQQLADEVRGYL	Query Match 65.7%; Score 2114; DB 16; Length 621; Best Local Similarity 63.1%; Pred. No. 1.4e-145; Matches 392; Conservative 102; Mismatches 123; Indels 4; Gaps	SEQUENCE 621 AA; 67959 MW; 69DABA88B22E8D4B CRC64;		16798: AAO08845.1:	complete genome sequence of vibil variations covers.	Choy H.B.;	Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	MCP6;	SEQUENCE FROM N.A.	[E] =	NCBI TaxID=672;	***	Barteria: Protechacteria: Gammaprotechacteria: Vibrionales:	Within this is	Deoxyxylulose-5-phosphate synthase.	3. Last	01-MAR-2003 (TrEMBLrel. 23, Last sequence update)	-2003 (TrEMBLrel. 23, Created)	i i	1
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Query Match
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Matches 383;
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Heidelberg J.F., Paulsen I.T., Nelson K.B., Gaidos B.J., Nelson W.C.
Heidelberg J.F., Paulsen I.T., Nelson K.B., Gaidos B.J., Nelson W.C.
Read T.D., Bisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,
Meyer T., Tsapin A., Scott J., Beanan M., Brinkac L., Daugherty S.,
DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
Madupu R., Peterson J.D., Umayam L.A., White O., Welf A.M.,
Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
Waeller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.;
"Genome sequence of the dissimilatory metal ion-reducing bacterium
Shewanella oneidensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8EGR9;
01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Deoxyxylulose-5-phosphate synthase.
DXS OR S01525.
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Alteromonadaceae; Shewane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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TDYPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHPAAGLGTVELTVALHY
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                                                                            Conservative
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                                                                                                                                                                     68083 MW;
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                                                                       Score 2042; DB 16;
Pred. No. 2.5e-140;
5; Mismatches 126;
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                                                                                                                      DB 16;
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                                                             STRAIN=O6:H1 / CFT073 / ATCC 700928;

MEDLINE=22388234; PubMede12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., &
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome
of uropathogenic Escherichia coli.;
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last amotation update)
1-deoxy-D-xylulose 5-phosphate synthase (EC 4.1.3.37).
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Aksoy S.;
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MEDLINE=22297718; Po
Akman L., Yamashita
                                                                                                                                                                                                                                     Wigglesworthia brevipalpis.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
                                                                               "Genome sequence of the endocellular flies, Wigglesworthia glossinidia."; Nat. Genet. 32:402-407(2002)
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SEQUENCE FROM N.A.

STRAIN=1330 / Biovar 1;

WEDLINB=22247741; PubMed=12271122;

WEDLINB=22247741; PubMed=12271122;

Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J. Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J., Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R., Daugherty S.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L., Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M., The Brucella suis genome reveals fundamental similarities betwee animal and plant pathogens and symbionts.";
                                                                                                                                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, 01-MAR-2003 (TrEMBLrel. 23, Deoxyxylulose-5-phosphate s)
                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
Brucellaceae; Brucella.
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01-MAR-2003 (TrEMBLrel. 23;
SEQUENCE FROM N.A.
STRAIN-TLS / ATCC 49652 / DSM 12025;
MEDLINE-22103685; PubMed=12093901;
Eisen J.A., Nelson K.E., Paulsen I.T.,
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InterPro; IPR005476; Transketolase C.
InterPro; IPR005476; Transketolase CR.
InterPro; IPR005474; Transketolase N.
Pfaa; PP02780; transketolase C; 1.
Pfam; PF02779; transketolase C; 1.
Pfam; PF02779; transket pyr; 1.
ITGRFAMs; TIGR00204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
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                                        FLKPLDTEIIDMAASRCTHIVTIEENSIIGGFGSNVVNYLHEAHPGIKCISFGLPDAFVT
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082676;
01-NOV-1996 (TrEMBLrel. 08, Created)
01-NOV-1996 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 23, Last annotation update)
1-deoxyxylulose 5-phosphate synthase.
Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Jamiids; Gentianales; Apocynaceae; Rauvolficideae; Vinceae;
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alkaloid-producing cells.*;

Plant Physiol Biochem 38:559-566(2000)

EMBL; AJ011840; CAA09804.2;

InterPro; IPR005477; Dxs.

InterPro; IPR005475; Transketclase_CR.

InterPro; IPR005475; Transketclase_CR.
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Q8DL74;
01-MAR-2003
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Makamira Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamot Makamira Y., Kaneko T., Sato S., Ikeuchi M., Kimura T., Kishida Y., Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Watsuno A., Nakazaki N., Shimpo S., Sugimoto M., Matsumoto M., Watsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
DNA Res. 9:123-130(2002).
EMBL; AP005371; BAC08174:1; -.
COMPLETE PROTECOME.
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Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
NCBI_TaxID=32046;
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YGVALMEEGWEPLEIGKGELLRSGEDLLLVAYGSMVYPAMQVAEILKEHGMSAAVINARF
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                                PGAAI-DPTLTALEIGKAEVRHHGSRIAILANGSMVTPAVEAGKQL----
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rynthases: differential regulation in shoots and apocaroten
recumulating mycorrhizal roots.";

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
REMBL, Ad430048; CAD22531.1; -.

R InterPro; IPR005476; Transketolase C.
R InterPro; IPR005476; Transketolase CR.
R InterPro; IPR005474; Transketolase CR.
R InterPro; IPR005474; Transketolase C.
R InterPro; IPR005474; Transketolase C.; 1.
Pfam; PF02790; transketolase C; 1.
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MLR-2003 (TrEMBLrel. 23, Last annotation update)
1-deoxy-D-xylulose 5-phosphate synthase 2 precursor.
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; endicotyledons; core endicots; Rosidae

eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae; Medicago.
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                                                        PLAYEGVPAFDPTKDFLPKAAPSPHPTYTEVFGRWLCDMAAQDBRLLGITPAMREGSGLV 353
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2; Mismatches 192; II
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EMBL; AJ42932: CAD22155.2; -.

EMBL; LPR005477; Dxs.

InterPro; IPR005476; Transketolase_C.

InterPro; IPR005475; Transketolase_C.

Pfam; PP027780; transketolase_C; 1.

Pfam; PP02779; transketolase_C; 1.

Pfam; PP02779; transket_Dyr; 1.

TIGRPAMS; TIGR00204; dxs; 1.

PROSITE; P908802; TRANSKETOLASE 2; 1.

PROSITE; P908802; TRANSKETOLASE 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eupatorieae; Stevia.
NCBI_TaxID=55670;
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                                                                                                                                                            TPDDKIIWDVGHQAYPHKILTGRRSKMHTIRKTSGLAGFFKKDESAHDAFGAGHSSTSIS
                                           ATLDGPATPVGALSGALSKLQASTKFRKLREAAKSITKQIGPQAHEVAAKVDEYARGMIS
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                                                                                                    PVGAMNNYLTKVLSSKFYSSVREESKKALAKM-PSVWELARKTEEHVKGMIV
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47.7%; Pred. No. 2.5e-96;
tive 108; Mismatches 193; I
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InterPro; IPR005476; Transketolase_CR.
InterPro; IPR005475; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
Pfam; PP02780; transketolase_C; 1.
Pfam; PP02779; transket byr; 1.
TIGREAMS; TIGR00204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
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Q8KZ13;
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Hamada T.,
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Bacteria; Proteobacteria; e
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01-OCT-2002 (TrEMBLrel. 22,
01-MAR-2003 (TrEMBLrel. 23,
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EMBL; AE008921; AAM48660.1; -.
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Beja O., Suzuki M.T., Heidelberg J.F., Nelson W.C., Pre
Hamada T., Eisen J.A., Fraser C.M., DeLong E.F.;
"Unsuspected diversity among marine aerobic anoxygenic
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                                                                                                                                                                                                                             YPLLKNIHTPADIRALSKDQLQQLADEVRGYLTHTVSISGGHFAAGLGTVBLTVALHYVF 66
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                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                             44.7%; Score 1437.5; DB 2;
47.6%; Pred. No. 3.4e-96;
tive 100; Mismatches 195;
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                                                                                    Query Match
Best Local Sim
Matches 302;
                                                                                                                                                                                              InterPro; IPR005477; Dxs.
InterPro; IPR005476; Transketolase_C.
InterPro; IPR005476; Transketolase_CR.
InterPro; IPR005474; Transketolase_N.
Pfam; PP02779; transketolase_C; 1.
Pfam; PP02779; transketolase_C; 1.
Pfam; PP02779; transket_Dyr; 1.
TIGRPAMS; TIGR00204; dxs; 1.
PROSITE; PS000801; TRANSKETOLASE_1; 1.
PROSITE; PS000801; TRANSKETOLASE_2; 1.
SEQUENCE 709 AA; 75747 MM; IPBA362A0DEDC6D3 CR
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Q9FSG2;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-CCT-2002 (TrEMBLrel. 2, Last annotation updat
1-D-desoxyxylulose 5-phosphate synthase (DXS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schaub P., Beyer P., Al-Babili S.;

"A cDNA encoding 1-D-descxyxylulose 5-phosphate synthase Narcissus pseudonarcissus L.";

Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ79019; CAC08458.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Narcissus pseudonarcissus (Daffodil).
Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
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Schaub P., Beyer F
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                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SAAHGFTVARDLGQDTGDAIAVIGDGSISAGMAYEALNNAGAEGRRXFVILNDNEMSIAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMTLPDRFIDQAAPDAMYADAGLTATDIAATALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DMLFALDRAGIAGEDGFTHAGAFDYSYMRCIPNMLIMAFADENECRQMLTTGFQHH-GPA 471
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AFRYPRGTGTGVSIPQEGELLQIGKGRIVRPGAEIALLSFGGHLAEALKAADLISAQGVD 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SVRYPRGKGPGAAIDPTLTALBIGKAEVRHHGSRIAILAWGSMVTPAVEA-----GKQLG 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVRFÄIDRAGLVGADGATHÄGÄFDIGFLTALPNMVVMÄAÄDEAELVHMITTAAAHDTGPI 468
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                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                44.68;
                                                                                       107;
                                                                                    Score 1435.5; DB 10;
Pred. No. 5.8e-96;
7; Mismatches 195; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta;
a; Asparagales; Amaryllidaceae;
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                                                                                          Indels
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                  C STRAIN=Cv. Yugoslavia; TISSUE=Root;
Wobbe K.K., Souret F.F., Shore K.A., Weathers P.J.;
Wobbe K.K., Souret F.F., Shore K.A., Weathers P.J.;
"Artemisia annua D-1-deoxyxylulose-5-phosphate synthase (dx. BMBL; AF182286; AAD56390.2; -.
R InterPro; IPR005476; Transketolase C. InterPro; IPR005476; Transketolase C. InterPro; IPR005476; Transketolase CR. R InterPro; IPR005476; Transketolase CR. R InterPro; IPR005476; Transketolase CR. R InterPro; IPR005476; Transketolase CR. R FinesPro; IPR005474; Transketolase C; 1.
R FinesPro; IPR005474; Transketolase C; 1.
R Ffam; PF02780; transketolase C; 1.
R Ffam; PF0279; transketolase C; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9SP65
Q9SP65;
01-MAY-2000
01-CCT-2000
01-CCT-2002
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01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
1-deoxy-D-xylulose-5-phosphate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Artemisia annua (Sweet wormwood).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=35608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asteridae; campanulids; Asterales; Asteraceae; Asteroideae;
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MEDLING=20026086; PubMed=10556522;
Miller B., Heuser T., Zimmer W.;
"A Synechococcus leopoliensis SAUG 1402-1
deoxyxylulose 5-phosphate synthase gene an
reading frames is functionally involved in
diphosphate synthesis.";
FEBS Lett. 460:485-490(1999).
[2]
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NCBI_TaxID=1140;
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Pred. No. 5.9e-96;
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Holtman C.K., Sandoval P., Chen Y., Socias T., Mohler B.

McMurtry S., Gonzalez A., Salinas I., Golden S.S., Youd.

"Synechococcus elongatus PCC 7942 cosmid 3E9.";

Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases

EMBL; X04616; CAD55646.1: -.
  Morinda citrifolia (Indian mulberry).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermacophyta; Magnoliophyta; eudicoty!edons; core eudicots;

Asteridae; lamiids; Gentianales; Rubiaceae; Rubioideae; Morinda.

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Pfam; PP02799; transketolase_C; 1.
Pfam; PP02799; transket_Dyr; 1.
TIGRPAMS; TIGR00204; dxs; 1.
PROSITE; PS00801; TRANSKETOLASE_1; 1.
PROSITE; PS00801; TRANSKETOLASE_2; 1.
SEQUENCE 722 AA; 77970 MW; 58231942EAF9C767 CR
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Han Y.S., Roytrakul S., Verberne M.C., Heijden, Rvd, Ver
"Cloning and characterization of a cDNA encoding 1-deoxy
phosphate synthase from Morinda citrofolia.";
Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF443590; AAL32062.1; -.
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Search completed: January 29, 2004, 15:54:02 Job time: 49.2142 secs

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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Result
No.
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WPI; 2002-452200/48.	Koffas M, Odom JM, Schenzle A;		(DUPO) DU PONT DE NEWOURS & CO E I.	01-SEP-2000; 2000US-229858P.		28-AUG-2001; 2001WO-US26827.		14-MAR-2002.		WO200220728-A2.		Methylomonas 16a.		nitrous oxide; terpenoid; animal feed; carotenoid; exopolysaccharide.	methane-containing environment; waste water treatment system; isoprenoid;	ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill;	pyrophosphate dependent phosphofrutokinase; nitrogen-containing compound;	methane; methanol; Embden-Meyerhof carbon flux pathway; 16s RNA;	High growth methanotrophic bacterial strain; Cl carbon substrate; enzyme;		High growth methanotrophic bacterial strain polypeptide #32.		27-AUG-2002 (first entry)		ABG61582;		ABG61582 standard; Protein; 394 AA.	1582	LT 1

ABK83261.

functional gene encoding in Embden-Meyerhof carbon pathway high growth methanotrophic bacterial strain, useful for producing the cell proteins, grows on a Cl carbon substrate, and comprises a grows a C1 carbon substrate, and comprises

Claim 11; Page 141-142; 157pp; English

protein and for the biotransformation of a nitrogen-containing compound, ce gr ammonia, nitrate, nitrite or nitrogen. It is also ussful for the groduction of a feed product comprising a protein, carbohydrates and a contribute in methane-containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are consistent. The bacterial strain of the invention can be used as a contribution of biomass including proteins, carbohydrates and contribution of biomass including proteins, carbohydrates and a wide variety of pigments (particularly for isoprenoid pigments for the conversion of the invention of terpenoid and compounds, useful as pigments and as monomers in polymeric contential strain production of exopolysaccharides at high levels.

Considerial strain production represent high growth methanotrophic constraints and as monomers in polymerial sequences ABG61591-ABG61590 represent high growth methanotrophic contents and methanotrophic constraints and methanotr The invention relates to a high growth methanotrophic bacterial strain, which grows on a C1 carbon substrate e.g. methane and methanol, and comprises a functional Embden-Meyerhof carbon flux pathway comprising a comprises a functional Embden-Meyerhof bosobofrutokinase enzyme or a 16s coding a pyrophosphate dependent phosphofrutokinase enzyme or a The bacterial strain is useful for the production of single cell strain proteins of the invention

Sequence 394 A.

Length 394;

S Дb S Đ, Ś ᅜ Ş B δ 밁 S D, Query Match Best Local S Matches 394 361 301 301 241 241 181 121 121 181 394; 61 6 Similarity MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCIAHHPEYAVVVMES AQFKPDDAGSLELVLQADQDAREVARDIIKTLVA QIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGH VILLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLT 180 MDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNBEVKFTDIAVIIERSM 360 QIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPBRFDSGVAPLDIFEVGH ASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATWMVKGLELIEACLLFNMEPD ASGGPFRRTPIBTLSSVTPDQAVAHPKWDMGRKISVDSATWMNKGLELIEACLLFNMBPD VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLT KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT KVAEFKORIAASPVADIKVLSGSEALOOVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES 100.0%; ilarity 100.0%; Conservative 0 0 Score 1985; DB 23; Pred. No. 1.8e-185; Mismatches 394 394 Indels 0 120 240 180 60 0

> Methylomonas 16a sp. D-1-deoxyxylulose-5-phosphate reductoisomerase

aquaculture; enzyme; D-1-deoxyxylulose-5-phosphate Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; fragrance; electro-optic Dxr.

Methylomonas 16a sp.

07-MAR-2002

04-SEP-2001; 2001WO-US27420

01-SEP-2000; 2000US-229858P 01-SEP-2000; 2000US-229907P

DUPO) DU PONT DE NEMOURS & CO Ø

Brzostowicz PC, Cheng Q Odom JM, Picataggio SK, ю Dicosimo DJ, Rouviere PE; Koffas M, Miller ES;

WPI; 2002-351711/38.

producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon

Claim 42; Page 112-114; 156pp; English

encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carl substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. D-1-deoxyxylulose-5-phosphate reductoisomerase (Dxr) enzyme used in the invention. The invention relates to a method for producing carotenoid compounds. The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule carbon

Sequence 394

S 밁 á 밁 S 쁑 á 밁 Matches Query Match Best Local : 121 181 121 394; 61 Similarity KVABFKORIAASPVADIKVISGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT QIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGH VILANKEALVMSGQI FMQAVSDSGAVLLP IDSEHNAI FQCMPAGYTPGHTAKQARRI LLT MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYSQCLAHHPEYAVVVMBS ASGGPFRRTPIBTLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIBACLLFNMSPD VILANKEAL VMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLT KVABPKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMBS Conservative 100.0%; Score 1985; DB 23; 100.0%; Pred. No. 1.8e-185; tive 0; Mismatches 0; Indels Length 0 120 300 120 60 240 240 180 180 0

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Matches 394
                                                                                                                                                    The present invention relates to a new nucleic acid molecule encoding an isoprenoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an isoprenoid compound biosynthetic enzyme, and for the invention are also useful for regulating isoprenoid biosynthesis in an organism and for production regulating isoprenoid biosynthesis in an organism and for producing recombinant organisms for producing various isoprenoid compounds. The mucleic acid is also useful for feed additive, for the production of keratemoids and their derivatives, isoprenoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 2 (ORF2) dxr (1-deoxyxylulose-5-phosphate reductoisomerase enzyme) protein of the invention, as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive; keratenoid; pigment; flavour; fragrance; open reading frame 2; ORF2; dxr; 1-deoxyxylulose-5-phosphate reductoisomerase enzyme.
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                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                    Claim 4; Page 68-70; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acid molecule encoding a isoprenoid biosynthetic enzyme, isolated from Methylomonas 16a, useful for the production of isoprenoid
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Mismatches 0;
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KVAEFKQRIAASPVADIKVESGSEALQQVATEENVDTVMAAIVGAAGLEPTLAAAKAGKT 120

Query Match

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                                                                             The invention relates to methods and materials for the production of isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS) activity or decaprenyl diphosphate synthase (DXS) activity, is useful for increasing production of CoQ(10) in a cell having endogenous DDS activity. This sequence represents a protein relating to the isoprenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity,
                                                             production
                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 32; 246pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          production of isoprenoids, especially CoQ(10)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jessen H,
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The invention relates to methods and materials for the production of isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS)
                                                                                                                                                                                                                                                                                                                                                                Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
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                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                          EFKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTVLL
                                                                                                                                                                                                                                                                                                                                          TIILGSTGSIGESTLDVVSRHPEKFRVFALAGHKQVEKLAAQCQTFHPEYAVVADAEHAA
                            KPDDAGSLELVLQADQDAREVARDIIKTL 392
                                                         QKPDFDRFFCLKLAYEAMNAGGAAPCVLNAANEAAVAAFLDGQIKFTDIAKTVAHCLSQD
                                                                               EKPDIKRFPCIRLAYEAIKSGGIMPTVINAANBIAVEAFINBEVKFTDIAVIIERSMAQF
                                                                                                                                        VVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGHMDF
                                                                                                                                                                                                GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIBACLLFNMEPDQIB
                                                                                                                                                                                                                           ANKETLVVSGALFMETARANGAAVLPVDSEHNAVFQVLPRDYTGRLNEHGIASIILTASG
                                                                                                                                                                                                                                                       ANKEAL VMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG
                                                                                                                                                                                                                                                                                 RLEALLKRDGTA-TOVLHGAQALVDVASADEVSGVMCATVGAVGLPSALAAAQKGKTIYL
                                                                                                                                                                                                                                                                                                                                                                  ICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESKVA
                                                                                                             VVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAYCLGLPERIDSGVGDLDFDALSALTF
                                                                                                                                                                      GPELTADLNTEDSITEDQAVKHPNWRMGRKISVDSATMMNKGLELIEAHWLFNCPPDKLE
 FSDGIGDIGGLLAQUARTRAQARAFIGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             53.0%;
                                                                                                                                                                                                                                                                                                                                                                                                 49;
                                                                                                                                                                                                                                                                                                                                                                                                Score 1052.5;
Pred. No. 3.7e.
49; Mismatches
   393
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                                                                                                                                                                                                                                                                                                                                                                                                 123;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isoprenoid
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                                                                                                                  304
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AAO21878 standard; Protein; 398

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13-SEP-2002 (first entry

Isoprenoid related protein sequence SEQ ID ö

decaprenyl Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; DXS; diphosphate synthase. DDS;

Escherichia coli

WO200226933-A2

04-APR-2002

28-SEP-2001; 2001WO-US30328

29-SEP-2000; 2000US-236580P

(CRGI) CARGILL INC

Gokarn æ Jessen H, Zidwick

WPI; 2002-416480/44

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ARACATIST Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10) useful for

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RESULT 7
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Best Local &
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                                                                                                                                                                                                      04-APR-2002
                                                                                                                                                                                                                                                                                                                                                               Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; decaprenyl diphosphate synthase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The
                                                                                    29-SEP-2000; 2000US-236580P
                                                                                                                                          28-SEP-2001; 2001WO-US30328
                                                                                                                                                                                                                                                         WO200226933-A2
                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoprenoid related protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA021885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
Les 219; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NLSVEEKMDMREPQCVDDVLSVDANAREVARKEVMRLAS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CKLSALTFAAFDYDRYFCLKLAMEAFEQGQAATTALNAANEITVAAFLAQQIRFTDIAAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NASASQMEVLIHPQSVIHSMVRYQDGSVLAQLGBPDMRTPIAHTMAWPNRVNSGVKPLDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SILLIGSGGPFRETPLRDLATMIPDQACRHPNWSMGRKISVDSATWMNKGLEYIEARWLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entry)
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Pred. No. 2e-93;
56; Mismatches 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to methods and materials for the production of isoprenoids. More particularly the invention provides isolated nucleic acids, substantially pure polypeptides, host cells, and methods for producing various isoprenoid compounds. The polypeptides are useful for the production of isoprenoids, especially CoQ(10). Expressing the pure polypeptides, which has 1-deoxyxylulose-5-phosphate synthase (DXS) activity, is useful for increasing production of CoQ(10) in a cell having endogenous DDS activity. This sequence represents a protein relating to the isoprenoid activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
                                                                                                           N. gonorrhoeae
                                                                                                                                        07-MAR-2003
                                                                                                                                                                                              ABP79699
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                          WO200279243-A2
                                                    Neisseria gonorrhoeae
                                                                                  Antibacterial;
                                                                                                                                                                   ABP79699;
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                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                                                                                                                                     PEVGHMDFEKPDLKRFPCLRLAYBAIKSGGIMPTVLNAANEIAVBAFLNEEVKFTDIAVI
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                                                                                                                                                                                                                                                                                              IERSMAQFKPDDAGSLELVLQADQDARSVARDIIKTLVA 394
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          398 AA;
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                                                                                infection; vaccine; gene therapy
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Pred. No. 2e-93;
6; Mismatches 118;
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               Antibacterial;
                                                                    07-MAR-2003
                                                                                              ABP80486;
                                                                                                                        ABP80486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence
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                                         gonorrhoeae
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                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                   VVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERPDSGVAPLDIFEVGHMDF
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                                                                                                                                                                                                                                                                                                 VVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAYCLGLPERIDSGVGKLDFGALSALTF 321
                                                                                                                                                                                                                                                                                                                                                      GPFLTTDLSTFDSITPEQAVKHPNWRMGRKISVDSATMANKGLELIEAHWLFNCPPDKLE
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                                                                                                                                                                                                                                                                                                                                                                                                            ANKETLVVSGALFMETARANGAAVLPVDSEHNAIFQVLPRDYTDRLNEHGIDSIILTASG
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               infection; vaccine;
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Pred. No. 3e-93
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New protein from Neisseria gonorrheae, medicament for treating or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                    VVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAYCLGLPERIDSGVGKLDFGALSALTF
                                                                                                                                 WIHPOSIIHSMVDYVDGSVLAQMGNPDMRTFIAHAMAWPERFDSGVAPLDIFEVGHMDF
                                                                                                                                                                                       GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELTEACLLFNMEPDQIE
                                                                                                                                                                                                               ANKETLYVSGALFMETARANGAAVLPVDSEHNAIFQVLPRDYTDRLNEHGIDSIILTASG
                                                                                                                                                                                                                                                                      RLEALLKRDGTA-TQVLHGAQALVDVASADEVSGVMCAIVGAAGLPSALAAAQKGKTIYL
                                                                                                                                                                                                                                                                                                                                                 ICILGATGSIGVSTLDVVARHEDKYQVVALTANGNIDALYEQCLAHHEEYAVVVMESKVA
                                                   QKPDFGRFPCLKFAYETINAGGAAPCVLNAANETAVAAFLDGQIKFTDIAKTVAHCLAQD
                                                                                                                                                          GPFLTTDLSTFDSITPEQAVKHPNWRMGRKISVDSATMANKGLELIEAHWLFNCPPDKLE
                                                                                                                                                                                                                                         ANKEAL VMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG
                                                                                                                                                                                                                                                                                                                          LTILGSTGSIGESTLDVVSRHPEKFRVFALAGHKQVEKLAAQCQTFRPEYAVVADAEHAA
 FSNGMGDIEGLLAQDARTRAQARAFIGTL
                        KPDDAGSLELVLQADQDAREVARDIIKTL 392
                                                                            EKPOLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSMAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                  411 AA;
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Pred. No. 3e-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
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LNQLVVSKLQPQKIHCIEDVLEVDKKARELSQSII
                                                                           IEEVGHMDEEKPDLKREPCLRLAYBAIKSGGIMETVLNAANEIAVEAFLNBEVKETDIAV 354
                                                                                                                          FNMEPDQIEVVIHPQSIIHSWVDYVDGSVLAQMGNPDMRTPIAHAMAMPERFDSGVAPLD
                                                                                                                                                             SKIVLTGSGGPFRYTPLEQFEQITPAQAVAHPNWSMGKKISVDSATMMKGLEYIEARWL
                                                                                                                                                                             RRILLTASGGPFRRTPIETLSSYTPDQAVAHPKWDMGRKISVDSATMYNKGLELIEACLL
                                                                                                                                                                                                                                                                                                  KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAALVGAAGLLPTLAAAKAGKT 120
                                                                                                                                                                                                                                                                                                                               MKKEVIIGSTGSIGTSTLSVITHNPDKYQVFALVGGRNVELMFQQCLTFQPSFAALDDDV 61
                                                                                                                                                                                                                                                                                                                                              MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
                       IIERSMAQFKPDDAGSLELVLQADQDAREVARDII
                                                                                                                                                                                                                    VILLANKEALVICGQLFIDAVRESQAQLLPVDSEHNAIFQSLPPEAQRQIGFCP-LSELGI 179
                                                                                                                                                                                                                                                                          AARMLAEKLKAHQ-SQTTVLAGQQAICELAAHPEADMVMAAIVGAAGLLPTLSAVKAGKR
                                                    FYQLNGLTFIEPDYQRYPCLKLAIDAFSAGQYATTAMNAANEIAVASFLDNKIKFTDIAR
                                                                                                          FNASAEEMEVIIHPQSIIHSMVRYIDGSVIAQMGNPDMRTPIAETMAYPSRTVAGVEPLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                         400 AA;
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53.2%;
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Pred. No. 4.1e-93;
58; Mismatches 109;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity, production of isoprenoids, especially CoQ(10)
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decaprenyl diphosphate synthase.
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242
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NASAEEMEVIIHPOSIIHSMVRYVDGSVITOMGNPDMRTPIAETMAYPHRTFAGVEPLDF
                                                                        LLANKBALVMSGQIFMQAVSDSGAVLLFIDSEHNAIFQCMP-----AGYTPGHTAKQAR 175
                                                                                                                                                                   AKILREKLIAHHI-PTEVLAGRRAICELAAHPDADQIMASIVGAAGLLPTLSAVKAGKRV
                                                                                                                                                                                                                        QNIVILGSTGSIGKSTLSVIENNPQKYHAFALVGGKNVEAMFEQCIKFRPHFAALDDVNA
                                                                                                                                                                                                                                                   KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; Protein;
               NMEPDQIEVVIHPQSIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDI
                                                      KIILIGSGGPFRYTPLEQFTNITPEQAVAHPNWSMGKKISVDSATMANKGLEYIEARWLF
                                                                                                             LLANKBSLVTCGOLFIDAVKNYGSKLLPVDSEHNAIFQSLPPBAQEKIGFCP-LSELGVS
                                                                                                                                                                                             VARFKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTV
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50.6%; Pre
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Pred. No. 1.1e
76; Mismatches
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                                                                                                                                                                                                                                                                               ; DB 23;
1.1e-89;
hes 111;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isoprenoid related protein sequence
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LLANKESLVTCGQLFIDAVKNYGSKLLPVDSEHNAIFQSLPPEAQEKIGFCP-LSELGVS 181
                                                                                                             AKILREKLIÄHHI-PTEVLAGRRÄICELÄÄHPDADQIMASIVGAAGLIPTISAVKAGKRV
                                                LLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMP-----AGYTPGHTAKQAR
                                                                                                                                                                 VABEKQRIAASPVADIKVLSGSBALQQVATLENVDTVMRAIVGAAGLLPTLAAAKAGKTV
                                                                                                                                                                                                                                                                               KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK 61
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... No. 1.1e-89;
... Mismatches 111.
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                                                                                                                                                                                                                                                                                                                                         DXR; reductoisomerase; enzyme; non-mevalonate isoprenoid; menaquinone; ubiquinone; virucide; ear infection; conjunctivitis; meningitis; pneumonia; conjunctivitis; bacteraemia; sinusitis;
                                                                                                                                                                                                                                                      09-AUG-2000; 2000US-223909P
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                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae
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The invention relates to modulating an activity of a DXR reductoisomerase enzyme of Haemophilus influenzae, comprising contacting the enzyme with a compound that modulates non-mevalonate isoprenoid biosynthesis - synthesis of menaquinone or ubiquinone. Compounds of the invention act as virucides. The method is useful for treating a mammal or mammalian tissue infected with H. influenzae having DXR reductoisomerase enzyme, e.g. a human or a domestic animal. In particular, the method is useful for treating ear infections, conjunctivitis, meningitis, pneumonia, conjunctivitis, bacteraemia, sinusitis, pleural empyema, endocardicis and epiglottitis. The current sequence represents the H. influenzae DXR reductoisomerase anzyme of treating earnesses. (e.g. ear infections or pneumonia)
modulator of its activity -Modulating Haemophilus influenzae DXR reductoisomerase enzyme activity, useful for treating mammals or tissues infected with H. influenzae (e.g. ear infections or pneumonia) by contacting the enzyme with a reductoisomerase enzyme polypeptide sequence.

Note: In the sequence listing, on page 40-44 of the specification, is given an amino acid sequence that is also described as SEQ ID 2, is the identifier of the current sequence. This sequence is given in record ABB09437, and contains the amino acids given in the current sequence but with a large insertion of extra amino acids that are no Claim 6(i); Page 5; 44pp; English. which

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
          Disclosure; Fig 27; 246pp; English
                                   production of isoprenoids, especially CoQ(10)
                                                 Substantially pure polypeptides having e.g., 1-deoxyxylulose-5-phosphate synthase activity,
                                                                                      WPI; 2002-416480/44.
                                                                                                               Gokarn
                                                                                                                                                              29-SEP-2000; 2000US-236580P
                                                                                                                                                                                      28-SEP-2001; 2001WO-US30328
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                                                                                                                                                                                                                                                                 Zymonas mobilis
                                                                                                                                                                                                                                                                                       Isoprenoid; CoQ(10); 1-deoxyxylulose-5-phosphate synthase; DXS; decaprenyl diphosphate synthase.
                                                                                                                                                                                                                                                                                                                            Isoprenoid related
                                                                                                                                                                                                                                                                                                                                                                               AA021879;
                                                                                                                                                                                                                                                                                                                                                                                                      AAO21879 standard; Protein;
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                                                                                                                                     (CRGI ) CARGILL INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMP-----AGYTPGHTAKQAR 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AKILREKLIAHHI-PTEVLAGRRAICELAAHPDADQIMASIVGAAGLLPTLSAVKAGKRV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMFTVLNAANEIAVEAFLNEEVKFTDIAVI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FKIKELTFIEFDFNRYFNLKLAIDAFAAGQYATTAMNAANBIAVQAFLDRQIGFMDIAKI
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                                                                                                             Jessen H,
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Pred. No. 1.1e-89;
76; Mismatches 111;
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                                                                                TPATPSSLEDVFAIDNEARIQAAALMESLPA
                                                                                                                    KPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                                                                                                                                                                    EKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSMAQF 363
                                                                                                                                                                                                                                           ILVHPQSVIHSMVEYLDGSILAQIGSPDMRTPIGHTLAMPKRMETPAESLDFTKLRQMDF 297
                                                                                                                                                                                                                                                                               VVIHPOSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERPDSGVAPLDIFEVGHMDF 303
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                                                                                                                                                            EAPDYERFPALTLAMESIKSGGARPAVMNAANETAVAAFLDKKIGFLDIAKIVEKTLDHY 357
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US-09-198-452A-362
US-09-198-452A-362
US-09-252-991A-17790
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US-09-252-991A-17607
US-09-252-991A-352-752
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US-09-252-991A-25375
US-09-252-991A-25556
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20932, A
20932, A
4916, Ap
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7199, Ap
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29, Appli
             7, Appli
22727, A
25556, A
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Sequence 21113, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: MARC J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND ACID SEQUENCES RELATING TO P.

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

PILE REFERENCE: 107196,136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR PILING DATE: 1998-02-18

PRIOR FILING DATE: 1998-07-27

INUMBER: OF SEQ ID NOS: 33142

SEQ ID NO 21113

LENGTH: 617

TYPES: PRT

CORGANISM: Pseudomonas aeruginosa

US-09-252-991A-21113

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Seguence 72, Appl	Sequence 25730, A	Patent No. 5460961	Sequence 29967, A	Sequence 4, Appli	Sequence 5, Appli	Sequence 4, Appli	Sequence 32789, A	Sequence 5834, Ap	Sequence 35, Appl	Sequence 36, Appl	Sequence 3, Appli	Sequence 4, Appli	Sequence 35, Appl	Sequence 3, Appli	Sequence 6, Appli	Sequence 37, Appl	Sequence 2, Appii

ALIGNMENTS

RESULT 1 US-09-252-991A-21113

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RESULT 3
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT TEILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7199
LENGTH: 398
TYPE: DEF
                               GÉNERAL INFORMÁTION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE,
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: MSUR14977
CURRENT APPLICATION NUMBER: US/09/491,362
CURRENT FILING DATE: 2000-01-26
CARLIER APPLICATION NUMBER: 60/118,349
EARLIER FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                           Sequence 7, Application US/09491362 Patent No. 6281017
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SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                           VGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIB 357
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56.7%; Pred. No. 3.4e
tive 58; Mismatches
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-874-562-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/09874562 Patent No. 6420159 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 7
                                                                                                                                            Matches 176;
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Best Local Similarity
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Croteau, Rodne
APPLICANT: Lange, Bernd
                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 13
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APPLICANT: Lange Bernd M.
TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR17549
CURRENT APPLICATION NUMBER: US/09/874,562
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR PILING DATE: 1000-01-26
PRIOR PILING DATE: 1000-01-26
PRIOR FILING DATE: 1099-02-03
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Pred. No. 1.6e-81;
1; Mismatches 131;
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/ Match 41.2%; Score 818.5; DB 4;
Local Similarity 44.6%; Pred. No. 1.6e-81;
les 176; Conservative 71; Mismatches 131;
                                          62 VABPKORIĄASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLIPTLAAAKAGKTV 121
                                                                                                                              KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK
INELKEALADLDY-KLBIIPGEQGVIEVARHPEAVTVVTGIVGCAGLKPTVAAIEAGKDI 121
                                                                                                                                                                                                        Score 818.5; DB 4
Pred. No. 1.6e-81;
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US-09-449-335-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method of determining the activity of INVENTION: 1-deoxy-D-xylulose-5-phosphate reductoisomerase TITLE OF INVENTION: 1-deoxy-D-xylulose-5-phosphate synthase FILE REFERENCE: 2020US CURRENT FAPLICATION NUMBER: US/09/449,335 CURRENT APPLICATION NUMBER: US/09/449,335 CURRENT FILING DATE: 1999-11-24 EARLIER APPLICATION NUMBER: DE 199 35 967.9 EARLIER FILING DATE: 1999-07-30 NUMBER OF SEQ ID NOS: 8 SOFTMARE: Patentin Ver. 2.1
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APPLICANT: Hain, Rudiger
APPLICANT: Martin, William
APPLICANT: Tietjen, Klaus
APPLICANT: Kloti, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 477
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PEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVI
                                          YDDIEIVIHEQSIIHSMIETQDSSVLAQLGWEDMRLFILYTMSWEDRVECSEVTWERLDL
                                                                                PDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAP---LDI
                                                                                                                          LTASGGAFRDWPVEKLKEVKVADALKHPNWNWGKKITVDSATLFNKGLEVIEAHYLFGAE
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                                                                                                                                                                                                                                                                                                                                                                                                   KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK 61
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APPLICANT: Levin, Joshua Z.
APPLICANT: Budziesewski, Gregory J.
APPLICANT: Budziesewski, Gregory J.
APPLICANT: Budziesewski, Gregory J.
APPLICANT: Budziesewski, Gregory J.
APPLICANT: Petter M.
TITLE OF INVENTION: Herbicide Target Genes and Meterite OF FILE REFERENCE: PB/5-30780A
CURRENT APPLICATION NUMBER: US/09/480,921B
CURRENT FILING DATE: 2000-01-11
NUMBER OF SEQ ID NOS: 29
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 477
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: Busch, Marco
APPLICANT: Hain, Rudiger
APPLICANT: Martin, William
APPLICANT: Tietjen, Klaus
APPLICANT: Aloti, Andreas
ITITLE OF INVENTION: Method o
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US-09-449-335-2
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US-09-480-921B-10
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Patent No. 6303365
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Best Local Similarity
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44.6%; Pred. No. 2.8e-81;
tive 69; Mismatches 127;
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APPLICANT: Potter, Sharon L.

APPLICANT: Wegritch, Lymette M.

TITILE OF INVENTION: Herbicide Target Genes an FILE REFERENCE: PB/5-30780A

CURRENT APPLICATION NUMBER: US/09/480,921B

CURRENT FILING DATE: 2000-01-11

NUMBER OF SEQ ID NOS: 29

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 41.0%; Score 914.5; DB 4; Best Local Similarity 44.3%; Pred. No. 6.1e-81; Matches 175; Conservative 71; Mismatches 132;
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LENGTH: 477
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ORGANISM: Arabidopsis thaliana
-09-449-335-2
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CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: DE 199 35 967.9
EARLIER FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 8
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                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Levin, Joshua Z. APPLICANT: Budziszewski, G
OTHER INFORMATION:
NAME/KEY: SITE
                                          NAME/KEY: SITE
LOCATION: (39)
                                                                                                           TYPE: PRT
ORGANISM: Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAP---LDI 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VAEFKORIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ITASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNME 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CKLGSLTPKKPDNVKYPSMDLAYAAGRAGGTMTGVLSAANEKAVEMFIDEKISYLDIPKV 431
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2 KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK 61

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Matches

Local Similarity hes 172; Conserv

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RESULT 9
US-09-491-362-2
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                                                                                                                                          SEQ ID NO 2
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Patent No. 628101
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Best Local :
                                 Query Match
                                                                                                                                                                                                                                                               APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: 1-DEGXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, AND
TITLE OF INVENTION: METHODS OF USE
FILE REFERENCE: WSUR14977
                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/491,362
CURRENT FILING DATE: 2000-01-26
EARLIER APPLICATION NUMBER: 60/118,349
EARLIER FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION:
NAME/KEY: SITE
                                                                                    LENGTH: 475
TYPE: PRT
ORGANISM: Mentha piperita
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KPISIVGSTCSIGTQTLDIVAENPDKFRVVALAAGSNVTLLADQVRRFKPALVAVRNESL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LDIFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTD
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                                                                                                                                                                                                                                                                                                                                                                                         Application
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37.3%; Score 741; DB 3; Length 47 ilarity 43.0%; Pred. No. 7.8e-73; Conservative 73; Mismatches 133; Indels
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Pred. No. 7.8e-81;
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                                   Length 475;
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CURRENT APPLICATION NUMBER: US/09/874,562
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 09/491,362
PRIOR FILING DATE: 2000-01-26
PRIOR APPLICATION NUMBER: 60/118,349
PRIOR FILING DATE: 1999-02-03
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Mentha piperita US-09-874-562-2
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US-09-874-562-2
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APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: 1-DEOXY-D-XYLULOSE-5-PHOSPHATE REDUCTOISOMERASE, TITLE OF INVENTION: METHODS OF USE FILE REFERENCE: WSUR17549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 37.3%; Score 741; DB 4; Similarity 43.0%; Pred. No. 7.8e-73;
                                                                                                                                                                                                                                                                                                  VABFKQRIAASPVADI-KVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
MEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMANPDMRTPIAHAMAWPER-PDSGVA--PL
                                                                                                                                                                                                                                                                                                                                                            KPISVIGSTGSIGTQTLDIVAENPDKFRIVALAAGSNVTLLADQ-KAFKPKLVSVKDESL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQC---MPAGYTPGHTAKQARRI 177
                                                                                                                       LLTASGGPERRTPIETLSSVTPDQAVAHPKWDWGRKISVDSATM-MNKGLELIEACLLEN 236
                                                                                                                                                                                                                                                                      ISELKEALAG--FEDMPEIIPGEQGMIEVARHPDAVTVVTGIVGCAGLKPTVÄAIEÄGKD
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                                                                         ILTASGGAFRDLPVEKLKEVKVADALKHSNWNMGKKNTVRLLQLFFNKGLEVIKAHYLFG
                                                                                                                                                                        IALANKETLIAGGPFVLPLAKKHNVKILPADSEHSAIFQCIQGLPEG------ALRRI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           73; Mismatches 133;
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US-09-252-991A-31862
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US-09-198-452A-362
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                                                                                                                                                                                            Sequence 31862, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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LENGTH: 340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 362, Application Patent No. 6559294
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELAT:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPBUTICS
EILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR APPLICATION NUMBER: US 60/094,190
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TITLE OF INVENTION: thereof and uses thereof, in ;
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT SPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    234 APERFASPRDGMDFSKKQTLEFFPVDEERFPSIRLAQQVLEKQGSSGSFFNAANEVLVRR 29:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138;
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US-09-252-991A-17790
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                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17790
LENGTH: 2285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 17790, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS:
SEQ ID NO 31862
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                                                                                                                                                               Query Match
                                                                                                                                                                                                 ORGANISM: Pseudomonas aeruginosa
-09-252-991A-17790
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILS REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR REPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                Local Similarity 22.8 tes 87; Conservative
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les 85; Conserv
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                           66 KQRIAASPVADIKVLSGSEAL---QQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTVL 122
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                                                                                             6 ILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYBQCLAHHPBYAVVVMBSKVABF 65
                                                            LIGAT---FVELLWRLAEHPDEAADFAFLAPRR-DA-----ASQPEPLVDV----VSLF 1550
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVQVGIAQAEACLRVRGMGDVGGSRAGQQRAHHAFQAFLLVQQVAG------QAQALA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -LLPTLAAAKAGKTVLLANKEALVMSGQIFMQAVSDSG-----AVLLPIDSEHNAIF 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGEVRÓRRMRRGLVEVARÍHPGEGIDHAQPFVQAVGAERPVVÁERAGVEVAAQADLGGIG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HP-----QSIIHSMVDYVDGSV-LAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFE- 297
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                                                                                                                              5.4%; Score 107; DB 4; Length 2285; 22.8%; Pred. No. 0.11; ative 51; Mismatches 137; Indels 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.6%; Score 111; DB 4; Length 671
21.1%; Pred. No. 0.005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58; Mismatches 139;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PAGYTPGHTAKQARRILLTASGGPFRRTPIETLSSV 197
Indels 106;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-428-517-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09428517
Patent No. 6251636
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/428,517
CURRENT FILING DATE: 1999-10-28
EARLIER APPLICATION NUMBER: 60/120,254
EARLIER FILING DATE: 1999-02-16
EARLIER APPLICATION NUMBER: 60/106,100
EARLIER FILING DATE: 1998-10-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tang, Li
TITLE OF INVENTION: RECOMBINANT OLEANDOLIDE POLYKETIDE
FILE REFERENCE: 30062-20029.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shah, Sanjay Krishnakant APPLICANT: McDaniel, Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Betlach, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 5.3%; Score 105.5; D
Local Similarity 17.8%; Pred. No. 0.41;
es 98; Conservative 76; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             3163 ESVLVHSAAGGVGMAAVQ-LARHNDA-EVFGTASKGKWDVLAAQGLDEEH-----IGSSR 3215
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                                                                                                                                                                                                                                                                                                                         62 VAREKORIAASPVADIKVLSGSBALQOVATLENVDTVMAA----
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                                                                                                                                                            DLGVVGADG-VPDIRYVAFDLARAGAERI------GOMLDEIMALFDAGVLRLPPL 3316
                                                                                                                                                                                                              ---IVGAAGLLPTLA-----AAKAGKTVLLANKEALVMSGQIF--MQAVSDSGAVLL--- 148
                                                                                                                                                                                                                                                                        TTEFEORFRAT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                  KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK 61
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                                                    RAWPVRRAHEAL ----
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                                                                                                        ---PIDSEHNAIFQCMPAGYTPGHTAKQARR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGALRVVVSSGEQLRITEDVR 1817
--- GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMN-KGLE----
                                                    ----RFVSQARHVGKVVLTVPAALDAEGTVLITGAGTLGAL
                                                                                                                                                                                                                                                                     SGGRGIDVVLNALSGDFVDASARLLREGGRFVEMGKTDIRT 3267
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     227
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	VAPLDIFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLAVAANEIA 338 	Qy 290 VAPLDIFEVGHM : : : Db 310QVIHL
	DQAVĖVGVTGDHDELRLHLALRGMHHRAGAALDAGRRĀLLVNSAAĒRLHRRRFAE 259 MEPDQIEVVIHPQSIIHSWVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSG 289	Db 205 DQAVEVGVTC Oy 237 MEPDQIEV Db 260 GEVQRMDVAA
	RILLTASGGPFR 18	110 128 159 188
	imilarity 20.3%; Score 99; DB 4; Length 482; conservative 57; Mismatches 156; Indels 124; Gaps 18; vvarhpdkyqvvallang-nidalyeqclahH:peyavvvmeskvaEFKQRI 69 : : : : : : : :	Query Match Best Local Similarity 20. Matches 86; Conservative Qy 20 VVARHPDKYQVVALT : : : Db 50 VVRQAGESVEALGLA Qy 70 AASPVADIKVLGGSE Qy AGPGEVDLHVLGGSE Db 110 AGPGEVDLHVLGGSE
DOMONAS	CCATION US/09252991A RUDENFIELD et al. NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS NUMBER: US/09/252,991A 1999-02-18 MMBER: US 60/074,788 1998-07-18 1998-07-27 1998-07-27 1998-07-27 1998-07-27 1998-07-27	WESULT 15 US-09-252-991A-20932 JSequence 20932, Application Pacent No. 6511795 JEDENERAL INFORMATION: APPLICANT: MARC J. Rubenfi ITILE OF INVENTION: MUCLEI FILL OF INVENTION: AERUGI FILL OF INVENTION: AERUGI FILL REFERENCE: 107196.136 CURRENT FILING DATE: 1999- PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR PILING DATE: 1998-07 INMERO OF SEQ ID NOS: 3314 SEQ ID NO 20932 JERGHI 482 TYPE: PRT ORGANISM: PSeudomonas aeru US-09-252-991A-20932
	VA 394 	Qy 383 EVARDIIKTLVA Db 3635 RALRDLVRGHVA
. 	AANEIAVEAFLNEEVKFTDIAVIIERSMAQFKPDDAGSLEIVLQADQDAR 382	Qy 333 Db 3604 RPSARAGTA
	FD-SGVAPLDIFEVGHXDFEKPDLKRFPCLRLAYBAIKSGGIMPTVLN 332 	Oy 286 FD-SGVAPLI : : Db 3544 MSRAGIAPM
		Qy 262 SVLAQMGNPD : : Db 3484 SAASMLGGPG
ا دیا	QIEVVIHPQSIIHSMVDYVDG ::: : : : : : : : : : : : :	228 - 3424 Þ
Ψ	VARHLVTEHDVRRLLLIVSRSGVAPDLAAELGALGAEVTVAACDVANRKALKALLEDIP 3423	Db 3366 VARHLVTEH

Search completed: January 29, 2004, 15:57:03 Job time : 13.3656 secs

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
   Result
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
Perfect score:
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                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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1985
Query
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                                                                                                                                                                                                                                                                                      / Cgn2_6/ptodata/1/pubpaa/US08_RUB_CUB_pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
/ Cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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/ Cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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/cgm2_6/ptodata/1/pubpaa/US06
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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6/ptodata/1/pubpaa/US06_NEW PUB.pep:*
6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
                                                                  SUMMARIES
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892.5	892.5	994.5	999.5	999.5	1007	1007	1042	1045	1045	1052.5	1215.5	1985	1985	1985	Score
45.0	45.0	50.1	50.4	50.4	50.7	50.7	52.5	52.6	52.6	53.0	61.2	100.0	100.0	100.0	Match
394	394	386	388	388	397	397	405	398	398	394	396	394	394	394	Match Length DB
12	12	12	12	12	12	12	12	12	12	12	12	11	10	10	B
US-10-381-779-121	US-10-381-779-103	US-10-381-779-97	US-10-381-779-116	US-10-381-779-101	US-10-381-779-120	US-10-381-779-99	US-10-381-779-122	US-10-381-779-118	US-10-381-779-100	US-10-381-779-119	US-10-381-779-117	US-09-941-947A-8	US-09-934-868-64	US-09-934-903-4	ID
Sequence 121, App	Sequence 103, App	Sequence 97, Appl	Sequence 116, App	Sequence 101, App	Sequence 120, App	Sequence 99, Appl		•	Sequence 100, App	•	Sequence 117, App	Sequence 8, Appli	Sequence 64, Appl	Sequence 4, Appli	Description

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61 KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120

45	44	43	42	41	40	<u>د</u> و	9. 8.	37	36	(J)	ω 4	(L)	32	3 1	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	
109	109.5	113.5	114	251	428.5	473	486	596	620	189	£91	9	169	692	697	718	721.5	729.5	731.5	798.5	798.5	813.5	814.5	817.5	818.5	818.5	818.5	886	886	
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426	6146	1073	425	98	177	368	356	1588	340	406	436	436	436	392	394	386	487	486	385	388	388	477	477	477	477	477	477	402	402	
12	15	15	12	12	12	12	12	12	12	12	12	12	4	Ç	15	12	12	12	12	12	12	14	9	14	12	10	ø	12	12	
US-10-369-493-21804	US-10-156-761-10436	-10-156-761	9-493-	US-09-864-408A-8646	US-10-032-395-1	US-09-882-227-500	US-10-381-779-130	US-09-925-778-2	US-10-289-762-362	US-10-381-779-126	US-10-381-779-127		US-09-712-363-258	US-09-738-626-5709	US-10-156-761-10100	US-10-381-779-124	US-10-259-194A-268	US-10-381-779-131	US-10-128-713A-4	US-10-381-779-125	US-10-381-779-98	US-10-047-412A-29	US-09-923-556-2	US-10-047-412A-10	US-10-381-779-128	US-09-987-025-2	US-09-923-556-6	US-10-381-779-123	US-10-381-779-102	
Sequence 21804, A	Sequence 10436, A	Sequence 12156, A	e 21773,	Sequence 8646, Ap	Sequence 1, Appli	e 5	Sequence 130, App	N	Sequence 362, App	e 12	e 12	Ø	e 258,	æ	1010	124,	268,	13	Sequence 4, Appli	129		2	ņ		Sequence 128, App	e 2	6, Ap	123,	Sequence 102, App	

ALIGNMENTS

US-09-934-903-4 RESULT 1

Sequence 4, Application US/09934903 Patent No. US20020102690A1

GENERAL INFORMATION:

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                                                                                                                                                                                                  ; OTHER INFORMATION: Amino acid sequences encoded by ORF2 US-09-934-903-4
                                                                                                                                                                                                                                                                                                                        APPLICANT: Cheng, Giong
TITLE OF INVENTION: Genes Involved in Isoprenoid Compounds Production
FILE REFERENCE: CL1646 US NA
CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: September 1, 2001
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 4
LENGTH: 394
                                                                                                  Matches
                                                                                                                           Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Koffas, Mattheos
APPLICANT: Odom, J. Martin
APPLICANT: Schenzle, Andreas J.
APPLICANT: No. US20020102690Alton, Kelley C.
APPLICANT: Tomb, Jean-Francois
APPLICANT: Rouviere, Pierre
APPLICANT: Rouviere, Stephen
                                                                                                                                                                                                                                                    ORGANISM: Methylomonas 16a FEATURE:
                                                                                                                                                                                                                                                                                                           TYPE: PRT
                                                                                             y Match 100.0%; Score 1985; DB 10; Length 394;
Local Similarity 100.0%; Pred. No. 7.2e-186;
hes 394; Conservative 0; Mismatches 0; Indels 0;
                           1 MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYZQCLAHHPEYAVVVMES 60
1 MKGICILGATGSIGVSTLDVVARHPDKYQVVALFANGNIDALYBQCLAHHPEYAVVVMES
                                                                                                Indels 0;
                                                                                                  Gaps
60
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APPLICANT: KOÉFAS, MATTHEOS

APPLICANT: Odom, James M

APPLICANT: Odom, James M

APPLICANT: Odom, James M

APPLICANT: Ochenzle, Andreas J

FILE REFERENCE: CL1596 US NA

CURRENT APPLICATION: DENITRITYING METHANOTROPHIC BACTERIAL STR

FILE REFERENCE: C11596 US NA

CURRENT APPLICATION NUMBER: US/09/934,868

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR FILING DATE: 2000-09-01

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Microsoft Office 97

SEQ ID NO 64

LENGTH: 394

TYPE: PRI

ORGANISM: Methylomonas 16a

FEATURE:

OTHER INFORMATION: Amino Acid Semigross encoded by DXB

FEATURE:
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US-09-934-868-64
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100
Best Local Similarity 100
Matches 394; Conservative
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            MDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSM 360
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                                                                                                                               ASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPD
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100.0%; Pred. No. 7.2e-186;
ive 0; Mismatches 0;
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CURRENT FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
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APPLICANT:
APPLICANT:
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APPLICANT: Cheng, Qiong
APPLICANT: Dicosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: ROUVIETE, PIETTE E.
TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Microsoft Office 97
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ORGANISM: Methylomonas 16a
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Miller, Edward S. Jr.
Odom, J. Martin
Picataggio, Steve
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                                                                                                 MDFEKPDLKRFPCLRLAYBAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIBRSM 360
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                  AQFKPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                                 MDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSM
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AQFKPDDAGSLELVLQADQDAREVARDIIKTLVA
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394
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RESULT 4
US-10-381-779-117
; Sequence 117, Application US/10381779

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APPLICANT: Gokarin, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR PILING DATE: 2001-09-28
PRIOR PILING DATE: 2001-09-28
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 119
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; ORGANISM: Pseudomonas aeruginosa
US-10-381-779-117
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                                                                                                                                                                                                                                                                                                                                                   Sequence 119, Application US/10381779 Publication No. US20030219798A1
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Best Local Similarity 64...
745; Conservative
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PRIOR PILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 117
LENGTH: 396
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
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FILE REFERENCE: 12904/002051
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOPTWARE: PastSEQ for Windows Version 4.0
LENGTH: 398
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; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-381-779-119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 100, Application US/10381779 Publication No. US20030219798A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 53.0
Best Local Similarity 55.9
Matches 216; Conservative
                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               305
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 VVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGHMDF
                                   61 KVABEKQRIAASEVADIKVISGSBALQQVATLENVDTVMAAIVGAAGLLETILAAAKAGKT 120
                                                                                                                                                             219;
61 S-AKILKTMIQQQGSRTEVISGQQAACDMAALEDVDQVMAAIVGAAGLLPTIAAIRAGKT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 EFKQRIAASPVADIKVISGSEALQQVATLENVDTVMAAIVGAAGILPTLAAAKAGKTVLL 123
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                                                                                                                                                           Conservative
                                                                                                                                                       52.6%; Score 1045; DB 12;
54.9%; Pred. No. 1.1e-93;
tive 56; Mismatches 118;
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                                                                                                                                                             Indels
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US-10-381-779-118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 52.6%;
Best Local Similarity 54.9%;
Matches 219; Conservative 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 118
LENGTH: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Escherichia coli
-10-381-779-118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
                               296 FEVGHMDFEKPDIKRFPCIRLAYEAIKSGGIMPTVLNAANBIAVZAFLNEEVKFTDIAVI 355
                                                                                                                                                  180 SILLTGSGGPFRETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIEARWLF
                                                                                                                                                                          176 RILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATWMNKGLELIEACLLF
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                                                                                                                                                                                                                                                             121 VILANKEALVMSGQIFMQAVSDSGAVILPIDSEHNAIFQCM--PAGYTPGHTAKQAR---
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                                                                                               NYEPDQIEVVIHPQSIHSMVDYVDGSVLAQWGNPDWRTPIAHAMAMPERFDSGVAPLDI 295
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 CKLSALTFAAPDYDRYPCLKLAMEAFEQGQAATTALNAANEITVAAFLAQQIRFTDIAAL
                                                                         NASASQMEVLIHEQSVIHSMVRYQDGSVLAQLGEPDMRTPIAHTMAWENRVNSGVKPLDF
                                                                                                                                                                                                                           ILLANKESLYTCGRLFMDAVKQSKAQLLFYDSEHNAIFQSLPQPIQHNLGYADLEQNGVV 179
                                                                                                                                                                                                                                                                                                                                                                            MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEA
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o. US20030219798A1
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Best Local Similarity
APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
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CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 122
LENGTH: 405
TYPE: PRT
ORGANISM: Pasteurella multocida
US-10-381-779-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
FILE REFERENCE: 12904/002US1
                                                              355 IIERSMAQFKPDDAGSLELVLQADQDAREVARDII 389
                                                                                                                                                                                           295 IFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAV 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VILIANKEALVMSGQIFMQAVSDSGAVILIPIDSEHNAIFQCMP-----AGYTPGHTAKQA 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 KVABFKQRIAASFVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLFTLAAAKAGKT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VLIANKEALVICGQLFIDAVRESQAQLLFVDSEHNAIFQSLPPEAQRQIGFCP-LSELGI 184
LNQLVVSKLQPQKIHCIEDVLEVDKKARELSQSII 399
                                                                                                                                                                                                                                                             FNASABEMEVIIHPQSIIHSMVRYIDGSVIAQMGNPDMRTPIABTMAYPSRTVAGVEPLD
                                                                                                                                                                                                                                                                                                FIMEEDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNEDMRTEIAHAMAWEERFDSGVAPLD
                                                                                                                                                                                                                                                                                                                                                                                              SKIVLTGSGGPFRYTPLEQFEQITPAQAVAHPNWSMGKKISVDSATMMNKGLEYIEARWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAKMLAEKLKAHQ-SQTTVLAGQQAICELAAHPEADMVMAAIVGAAGLLPTLSAVKAGKR 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MKKIVILGSTGSIGTSTLSVITHNPDKYQVFALVGGRNVELMFQQCLTFQPSFAALDDDV 66
                                                                                                                             FYQLNGLTP1EPDYQRYPCLKLAIDAFSAGQYATTAMNAANEIAVASFLDNKIKFTDIAR
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lo._US20030219798A1
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234

294

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PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER: OF SEQ ID NOS: 190
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120
LENGTH: 397
TYPE: PRT
ORGANISM: Haemophilus influenzae
US-10-381-779-120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT ; ORGANISM: Haemophilus influenzae US-10-381-779-99
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US-10-381-779-120
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LENGTH: 397
Query Match
Best Local Similarity
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PRIOR FILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
                                                                                                                                                                                                                                                                                    APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gokarn, Ravi R APPLICANT: Jessen, Holly
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50.7%;
Score 1007; DB 12; Pred. No. 6e-90;
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RESULT 11
US-10-381-779-101
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                                                                                                                                                                                                                                                                                 Best Local
Matches 19
                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
FITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/602US1
CURRENT EPPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
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PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
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PRIOR FILING DATE: 2001-09-28
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Zymonas mobilis
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184 GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMYNKGLELIEACLLFNMEPDQIE 243
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                                                                                                                                                                   EFKORIAASEVADIKVISGSEAIOOVATIENVOTVMAAIVGAAGILPTIAAAKAGKTVIL 123
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                                                                                ANKEALVMSGQIFMQAYSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG 183
                                                                                                                                                                                                        VTVLGATGSIGHSTLDLIERNLDRYQVIALTANRNVKDLADAAKRTNAKRAVIADPSLYN 66
                                                         ANKESIVSAGGIMIDAVREHGTTLLÞVDSBHNÁIFQCF----PHHNRDYVRRÍIITÁSG 177
                                                                                                                                 DIXEALAGS - -- SVEAAAGADALVEAAMM-GADWTMAAIIGCAGLKATLAAIRKGKTVAL
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p. US20030219798A1
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                                                                                                                                                                                                                                                                             50.4%; Score 999.5; DB 1 ilarity 50.9%; Pred. No. 3.2e-89; Conservative 74; Mismatches 109
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RESULT 13
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CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR PILING DATE: 2001-09-28
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 190
SEQ ID NO 116
SEQ ID NO 116
LENGTH: 388
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US-10-381-779-116
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
EILE REFERENCE: 12904/002US1
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Local Similarity 50.9%;
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                                                                                                                                                                                    EKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFINBEVKFTDIAVIIERSMAQF 363
                                                                                                                                                                                                                                                         VVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAMPERFDSGVAPLDIFEVGHMDF 303
                                                                                                                                                                                                                                                                                                                                                                                       ANXESTVSAGGEMIDAVREHGTTLLPVDSEHNAIFQCF----PHHNRDYVRRIIITASG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EFKORIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGILPTLAAAKAGKTVLL 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EKPDIKRFPCIRLAYEAIKSGGIMPTVINAANBIAVEAFINEEVKFTDIAVIIERSMAQF 363
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                                                                         TPATPSSLEDVFAIDNEARIQAAALMESLPA 388
                                                                                                               KPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                                                                                                                                                                                                                                                                                                                 GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMANKGLELIEACLLFNMEPDQIE 243
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                                                                                                                                                       EAPDYERFPALTLAMESIKSGGARPAVMNAANEIAVAAFLDKKIGFLDIAKIVEKTLDHY 357
                                                                                                                                                                                                                                ILVHPQSVIHSMVEYLDGSILAQIGSPDMRTPIGHTLAWPKRMETPAESLDFTKLRQMDF
                                                                                                                                                                                                                                                                                                              GPFRTTSLAEMATVTPERÄVQHPNWSMGAKISIDSATMMNKGLELIEAYHLFQIPLBKFE 237
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Pred. No. 3.2e-89;
4; Mismatches 109; Indels 9;
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APPLICANT: Gokarn, Ravi R
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Jessen, Holly
APPLICANT: Jedwick, Mary Jo
TITLE OF INVENTION: Isoprenoid Production
FILE REFERENCE: 12904/020US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT PILING DATE: 2003-03-28
FRIOR APPLICATION NUMBER: PCT/US01/30328
FRIOR FILING DATE: 2001-09-29
PRIOR PILING DATE: 2000-09-29
NUMBER OF SEQ ID MOS: 190
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 97
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               APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Mary Jo
APPLICANT: Zidwick, Mary Jo
TITLE OF INVENTION: Isopremoid Production
FILE REFERENCE: 12904/002US1
CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILLING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR APPLICATION NUMBER: PC7/US01/30328
PRIOR APPLICATION NUMBER: 60/236,580
PRIOR PILING DATE: 2000-09-29
PRIOR FILING DATE: 2000-09-29
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Best Local Sim
Matches 203;
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                                                                                                                                                                                                                                                                  APPLICANT: Gokarn, Ravi R
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SEQ ID NOS:
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D. US20030219798A1
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CURRENT APPLICATION NUMBER: US/10/381,779
CURRENT FILING DATE: 2003-03-28
PRIOR APPLICATION NUMBER: PCT/US01/30328
PRIOR FILING DATE: 2001-09-28
PRIOR PELICATION NUMBER: 60/236,580
PRIOR ETLING DATE: 2000-09-29
PRIOR ETLING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 199
SOFTMARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 121
SEQ ID NO 121
LENGTH: 394
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                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Synechocystis sp. PCC 6803
US-10-381-779-121
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Publication No. US20030219798A1
GENERAL INFORMATION:
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Best Local Similarity 47.3%;
Matches 183; Conservative (
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Best Local '
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Best Local Similarity
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APPLICANT: Jessen, Holly
APPLICANT: Zidwick, Kary Jo
TITLS OF INVENTION: Isopremoid Production
FILB REFERENCE: 12904/002US1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 VILANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCM---PAGYTPGHTAKQARRI 177
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61 KVAEFKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
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                                                                                         MKGICIIGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANBIAVEAFLNEEVKFTDIAVIIE 357
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                                                  VKRISILGSTGSIGTQTLDIVTHHPDAFQVVGLAAGGNVALLAQQVAEFRPEIVAIRQAE 61
                                                                                                                                                            45.0%; Score 892.5; DB 12; Length 394;
47.3%; Pred. No. 1e-78;
ative 63; Mismatches 128; Indels 13;
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                                                                            VGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIE 357
                                                                                                                  DYDHIDIVIHPQSIIHSLIEVQDTSVLAQLGWPDWRLPLLYALSWPERIYTDWEPLDLVK 293
                                                                                                                                                                               KTCDLYVGQNTASPDLETILAADQWAR 380
                                                           AGSLSFREEDHDKYPCMQLAYGAGRAGGAMPAVLNAANEQAVALFLQEKISFLDIPRLIE 353
                                                                                                                                                                                                             LLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATYMNKGLELIEACLLFNM 237
                            RSMAQFKPDDAGS -- LELVLQADQDAR 382
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Search completed: January 29, 2004, 16:21:15 Job time: 27.8953 secs

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Result
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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246 VVIHPQSVIHSMVDYVDGSVIAQLGNPDMRTPISYAMAWPERIDSGVSPLDMFAVEKLDF 305 304 EKPDLKRFPCLRLAYBAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSMAQF 363 :- - - - - - - -	ANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG 1	4 CILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESKVA 63 :	y-d-xylulose 5-phosphate reductoisomerase PA3650 [imported] - Pseudomonas aeruginos ies: Pseudomonas aeruginosa i.15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 ssion: BB3188

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C;Date: v.
C;Accession: bv.
C;Accession: bv.
R;Parkhill, J.; Acht...
R;Parkhill, J.; Jagels, K.,
; Holroyd, S.; Jagels, K.,
; Holroyd, S.; Jagels, K.,
Complete DMA seque
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R.Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete ganome sequence of Escherichia coli A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64741
A;Status: nucleic acid sequence not shown; translation not A;Molecule type: DNA
A;Residues: 1-398 <BLAT>
                                                                                                                   C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997
C;Accession: E64741
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A;Experimental source: serogroup
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B82000
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Pred. No. 9.5e-
49; Mismatches
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                                                                                                                                ftext_change 01-Mar-2002
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                                                                                                           V.; Riley,
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Rajandream,
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erfamily: conserved hypothetical protein HI0807
words: nucleotide binding; P-loop
-119/Region: nucleotide-binding motif A (P-loop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ss-references: GB:AE000126; GB:U00096; NID:g1786358; PIDN:AAC73284.1; PID:g1786369; erimental source: strain K-12, substrain MG1655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /ara, N.; Yasunaga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ession: G90650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          xy-D-xylulose 5-phosphate reductoisomerase cies: Escherichia coli
                                                                                                                                                                                                                               erfamily:
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ss-references: GB:BA000007; PIDN:BAB33598.1; PID:g13359631; erimental source: strain O157:H7, substrain RIMD 0509952
                                                                                                                                                                                                                                                                                                                                               ecule type:
                                                                                                                                                                                                                                                                                                                                                                                     ession: G90650
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le: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7
erence number: A99629; MUID:21156231; PMID:11258796
                                                                                                                                                                                                                                                      ECs0175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T.; Makino, K.; Ohnishi, M.;
N.; Yasunaga, T.; Kuhara, S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                             11-22, 2001
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                          KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
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S-AKLLKTMLQQQGSRTEVLSGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKT
                                                                                               MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYBQCLAHHPBYAVVVMES 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVI
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Pred. No. 3.5e-71;
6; Mismatches 118;
                                                                                                                                                                            Pred.
                                                                                                                                                                                            Score 1044;
                                                                            VRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEA
                                                                                                                                                       Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kurokawa, K.; Ishii,
Shiba, T.; Hattori,
                                                                                                                                                                            No. 4.2e-71;
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M.; Shinagawa,
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A; Gene:
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A;Cross-references: GB:AE005174; NID:g12512898; PIDN:AAG54475.1;
A;Cross-references: GB:AE005174; NID:g12512898; PIDN:AAG54475.1;
A;Cross-references: GB:AE005174; NID:g12512898; PIDN:AAG54475.1;
A;Cross-references: GB:AE005174; NID:g12512898; PIDN:AAG54475.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Genome sequence of enterohemorrhagic Escherichia coli
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: G85501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, Nature 409, 529-533, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-2001
C;Accession: G85501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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IERSMAQFKPDDAGSLELVLQADQDAREVARDIIKTLVA 394
                                                      CKLSALTFAAPDYDRYPCLKLAMEAFEQGQAATTALNAANEITVAAFLAQQIRFTDIAAL
                                                                                                                        NMEPDQIEVVIHPOSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDI
                                                                                                                                                                                                                    RILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLF
                                                                                                                                                                                                                                                                 ILLANKESLYTCGRLFMDAVKQSKAQLLPVDSEHNAIFQSLPQPIQHNLGYADLEQNGVV
                                                                                                                                                                                                                                                                                            VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCM--PAGYTPGHTAKQAR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                               MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYBQCLAHHPBYAVVVMBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLF
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                                                                                        FEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVI
                                                                                                                                                                                                SILLTGSGGPFRETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIEARWLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SILLTGSGGPFRETPLRDLATMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIEARWLF
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ilarity 54.9%;
Conservative :
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Pred. No. 4.2e-71;
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                                                                   09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change ssion: AF0529 iil, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowdonle, S.; O'Gaora, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; e: Complete genome sequence of Meisseria meningitidis serogroup B rence number: A81000; MUID:20175755; PMID:10710307 ssion: A81229
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   413, 848-852, 2001

YES: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
Complete genome sequence of a multiple drug resistant
ence number: AB0502; MUID:21534947; PMID:11677608
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cimental source: serogroup
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Pred. No. 7.6e
                                                                                        K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Davis, P.; Davies, R.M.; Dowd, L.; White, N
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                    Skelton, J.; Steven Salmonella enterica
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A;Gene: dxr
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A;Status: preliminary
A;Nolecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-398 <PAR>
A;Cross-references: GB;AL513382; PIDN:CAD08678.1; PID:g16501501; GSPDB:GN00176
C;Genetics:
                                                                                                                                                                                                          Nature 406, 477-483, 2000

A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: D82099

A;Status: preliminary

A;Molecule: type: DNA

A;Residues: 1-402 <HEI>
A;Cross-references: GB:AB004297; GB:AB003852; NID:g9656810; PIDN:AAF95398.1; GSPDB:GN001

A;Experimental source: serogroup O1; strain N16961; biotype El Tor

C;Genetics: A;Gene: VC2254

A;Map position: 1

C;Superfamily: conserved hypothetical protein HI0807
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                                                                                                         51.5%; Score 1023; DB 2; larity 52.7%; Pred, No. 1.6e-69; Conservative 65; Mismatches 103:
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cies: Yersinia pestis
e: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
es: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
ession: AG0128
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chill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, Khill, J.; Wren, B.W.; Chonson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, Carlon, J.; Samonds, M.; Skelton, J.; Samonds, R.; Shmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barre e 413, 523-527, 2001
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51; Mismatches 120;
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R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, B.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Lit, Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.; Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: A64014
           \lambda_iTitle: The genome sequence of the plant pathogen Xylella fastidiosa. \lambda_iReference number: A82515; MUID:20365717; PMID:10910347 \lambda_iNote: for a complete list of authors see reference number A59328 below
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C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 29-Sep-1999
                                                      R; anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Nature 406, 151-157, 2000
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                                                                                                  1-deoxy-D-xylulose 5-phosphate reductoisomerase XF1048 [imported] - Xylella
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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                                                                                                                                                                                                                                                                                       FEVGHMDFEKPDLKR:PCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVI
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6; Mismatches Ill;
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                                                                                                                                                               : 25-Apr-1997 #sequence_revision
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                                         rence number: S74322; ssion: S76331
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                                                          MUID:97061201;
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                                                             PMID:8905231
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co, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, B.; Nakamura, Y.; Miyajima, Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Ya. J. 109-136, 1996
s: Sequence analysis of the genome of the unicellular cyanobacterium Synechocy.
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ors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigre M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E. ors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. ues, V.; Ross, A.J. de M.; de Rossa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki ors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva Jr.; Wah.; da Silva Jr.; Wah.; Jako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zenence number: A59328
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C;Species: Buchnera sp.
C;Species: Buchnera sp.
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: P84957
C;Accession: P84957
R;Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
Nature 407, 81-86, 2000
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A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C;Superfamily: conserved hypothetical protein H10807
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A;Experimental source: strain APS
C;Genetics:
A;Gene: dxr; BU235
C;Superfamily: conserved hypothetical protein
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A;Molecule type: DNA
A;Residues: 1-398 <STO>
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Best Local S
Matches 182
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                                               VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTP--GHTA---KQAR
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                                                                                  SAHILRKKLKHSKI-NTQVLTGEKDICALAALEETDHVISAIVGMAGLLPTLSAIHAGKT
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47.3%; Pred. No. 1.1e-59;
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Pred. No. 1.4e-59;
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T 15
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A;Gene: CC1917
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A;Molecule type: DNA
A;Residue: 1-399 <STO>
A;Cross-references: GB:AE005673; NID:gl3423370; PIDN:AAK23892.1; GSPDB:GN00148
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Best Local Sim
Matches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RALSO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DXR_RALSO
Q8XZI5;
28-FEB-2003
                                                                                                   Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L. Chandler M., Choisen M., Claudel-Renard C., Cunnac S., Deman Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex Siguier P., Thebault P., Whalen M., Wincker P., Levy M., Weissenbach J., Boucher C.A.;
"Genome sequence of the plant pathogen Ralstonia solanacearu Nature 415:497-502(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (Directorisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase).

DXR OR RSC1410 OR RS05282.
                                                                                                                                                                                                                                                                                                                         MEDLINE=21681879;
                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. STRAIN=GMI1000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burkholderiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria; Betaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia solanacearum (Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isoprene biosynthesis; Oxidoreductase; NADP; Complete proteome
NP_BIND 10 17 NADPH (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGRFAMS;
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InterPro; IPR003821; E
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=305;
  of 1-deoxy-D-xyluiose-5-phosphate (DXP) to 2
4-phosphate (MSP) (By similarity).
CATALYTIC ACTIVITY: 2-C-methyl-D-exythritol
                                                                                  FUNCTION: Catalyzes the NADP-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; AE004785; AAG07038.1;
E83188; E83188.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVTAVESLIDQVLAADRRARSVA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORPDEGREPCLELASQAAETGGSAPAMLNAANEVAVAAFLERHIRESDIAVIIEDVLNEE 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EKPDIKRFPCIRIAYEAIKSGGIMPTVINAANBIAVEAFINEEVKFTDIAVIIERSMAQF 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GPFRRTPIETLSSVTPDQAVAHPXWDWGRKISVDSATWYNKGLELIEACLLFNWEPDQIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESKVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPFRETPLEQLASVTPEQACAHPNWSMGRKISVDSASMMNKGLBLIEACWLFDAQPSQVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTFGHTAKQARRILLTASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALQGSLAAAGIR-TRVLFGEQALCEVASAPEVDMVMAAIVGAAGLPSTLAAVEAGKRVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTVLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISVLGATGSIGLSTLDVVQRHPDRYEAFALTGFSRLAELEALCLRHRPVYAVVPEQAAAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                         PubMed=11823852;
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8.
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Pred. No. 9.3e
18; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  solanacearum)
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                                                                                                                                     Ralstonia solanacearum. *;
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.3e-80;
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                                                        rearrangement and reduction
) to 2-C-methyl-D-erythritol
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        4-phosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (EC 1.1.1.267) (DXP
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                                                                                                                                                                                                                  S., Demange N.,
W., Schiex T.,
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                                                                                                           15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
DXR OR VV11866.
                                                                                                                                                        Q8DBF5;
15-SEP-2003
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ry Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a cetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-entities.
Rhee J.H., Ki
                                                                      3acteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                    DXR VIBVU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAMAP; MF_00183; -; :
InterPro; IPR003821;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ÷
                                                                                                   Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF02670; DXP_reductoisom; 1.
FIGRFAMs; TIGR00243; Dxr; 1.
                              EQUENCE FROM N.A.
                                                        CBI_TaxID=672;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     = 1-deoxy-D-xylulose 5-phosphate + NADPH.
PATHWAY: Nonmevalonate terpenoid biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                      240
                                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                                                                                                                         237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
                                                                                                                                                                                                                                                                                                                                                                       HMDEEKPDLKREPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERS
                                                                                                                                                                                                                                                                                                                                                                                                                           DQIEVVIHPQSIIHSMVDYVDGSVLAQMCNPDMRTPIAHAMAWPERFDSGVAPLDIFEVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIBACLLFNMEP
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                                                                                                                                                                                                                                                                                                                    MAQEKPDDAGSLELVLQADQDAREVARDII
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                                                                                                                                                                                                                                                                                                                                                                                                         ERLEVLIH POSVIH SMVAYDDGS VLAQLGN PDMRTP LAYGLAY PERIEAGVPLLDLAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMRITVIGATGSIGDSTLDVVRRHPDRYRVFALTANTQVDKLAALCRVFRPAMAVVGSAT
 Kim S.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             41763 MW;
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 Chung
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                                                                                      Gammaproteobacteria;
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S
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Pred. No. 6.7e-71;
9; Mismatches 109;
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; 5A995A7C8FF32E9D CRC64;
    Z.
   J.J.,
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                                                                                                                                 reductoisomerase)
   Y.H.,
                                                                                                                                             (EC 1.1.1.267)
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   Jeong
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DXR NEIMA ID DXR NEIMA ID DXR NEIMA ID DXR NAIMA AC Q9JX3 AC Q9JX3 AC Q9JX 16-OC DT 16-OC DT 28-FE DE 1-dec DB reduc GN DXR C GN Neiss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Choy H.E.;
"Complete genome sequence Submitted (DEC-2002) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1
                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HAMAP; MF_00183; -;
InterPro; IPR003821;
Pfam; PF02670; DXP_re
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            reductoisomerase) (1-deoxyxylulose-5-phosphate DXR OR NMA0083.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isoprene biosynthesis; Oxidoreductase; NADP; Complete proteome.
NP_BIND 7 14 NADPH (POTENTIAL).
SEQUENCE 402 AA; 43352 MW; 13095814BF685BAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mplete genome sequence of Vibrio vulnificus CMCP6.";
mitted (DEC-2002) to the EMBL/GenBank/DDS databases.
FUNCTION: Catalyzes the NADP-dependent rearrangement and
of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-
4-phosphate (MEP) (By similarity).
CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate
= 1-deoxy-D-xylulose 5-phosphate + NADPH.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; s
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                                                                                                                                                                                                                             DFTQVGELTFLQPDFERYPCLALAIEACYLGQHATTTLNAANEVAVAAFLARQIKFTDIA
                                                                                                                                                                                                                                                        DIFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANBIAVBAFLNBEVKFTDIA
                                                                                                                                                                                                                                                                                                           LENMEPDQIEVVIHPQSI IHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPL
                                                                                                                                                                                                                                                                                                                                   VSHILLTGSGGPFRYTDVAELEAVTPEQAIAHPNWSMGPXISVDSATMNKGLEYIEAKW
                                                                                                                                                                                                                                                                                                                                                        ARRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KVAEFKORIAASPVA-DIKVISGSEALQQVATIENVDTVMAAIVGAAGILPTLAAAKAGK 119
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                                                                                                          STANDARD;
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Pred. No. 8.9e-69;
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A arkhill J., Achtman M., James K.D., Bentley S.D., Churcher C. Lee S.R., Morelli G., Basham D., Brown D., Chillingworth T., vvies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holr and the second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second second sec
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MAP; MF 00183; -; 1.

iterPro; IPR003821; DXP redisomrase.
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@RAIN=Z2491 / Ser
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BIND 9 16 NADPH (POTENTIAL).
QUENCE 394 AA; 41912 MW; B5D361B224806D6B CRC64;
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CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+) = 1-deoxy-D-xylulose 5-phosphate + NADPH.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; second
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Ms; TIGR00243; Dxr; 1.
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KPDDAGSLELVLQADQDAREVARDIIKTL
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                                                                                                                                                                                                                                                                                                                                                                                                                       GPFRRTPIBILSSVIPDQAVAHPKWDMGRKISVDSAIMMNKGLELIEACLLFNWEPDQIE
                                                                                                GPFLTADLNTFDSITEDQAVKHPNWRWGRKISVDSATWANKGLELIEAHWLFNCPPDKLE
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Pred. No. 4.1e-68;
9; Mismatches 123;
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Q87ME3;
15-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K., Iljima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S., Yasunaga T., Honda T., Shinagawa H., Hattori M., Ilda T.; Yasunaga T., Honda T., Shinagawa H., Hattori M., Ilda T.; "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism distinct from that of V. cholerae."; Lancet 361:743-749(2003).

Lancet 361:743-749(2003).

-i- CHONTION: Catalyzes the NADP-dependent rearrangement and reduction of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrit of 4-phosphate (MEP) (By similarity).

-i- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(1-1-CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADPH.

-i- CATALYTIC NORMEY - Phosphate + NADPH.

-i- PARHWAY: Nonmevalonate terpenoid biosynthesis pathway; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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15-SEP-2003 (Rel.
15-SEP-2003 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                HAMAP; MF_00183; -; 1.
Isoprene biosynthesis; Oxidoreductase; NADP; (NP_BIND 7 14 NADPH (POTENTIAL)
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                      LEYIEAKWLENAARDQLKVIIHEQSVIHSWVQYRDGSVLAQWGEEDMATEIALTMSYPSR
                                                         LELIEACLLENMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPER
                                                                                                                                                                  RVILLANKEALVMSGQLFIDAVEQYGAELLPVDSEHNAIFQCLP-
                                                                                                                                                                                     TVLLANKEALVMSGQI FMQAVSDSGAVLLPIDSEHNAI FQCMPAGYTPGHTAKQAR----
                                                                                                                                                                                                                                     AAVALQSEIHTISP--WTEVLGGVDALCHVASLEEVDSVMAAIVGAAGLLPTMAAVKAGK
                                                                                                                                                                                                                                                                     KVAEFKQRI-AASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGK
                                                                                               {\tt RCNLDEHGISSILLTGSGGPFRYADIADLDSVTPAQAIAHPNWSMGPKISVDSATMMNKG}
                                                                                                                                                                                                                                                                                                          MOKLTILGATGSIGASTEKVVEQNPELFSVVALAAGTNVEKMVALCROWQPKFAVMADKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2210633 / Serotype O3:R
08454; PubMed=12620739;
                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42, Created)
42, Last sequence update)
42, Last sequence update)
42, Last annotation update)
42, Est annotation update)
65-phosphate reductoisomerase (EC 1.1.1.267) (D)
61-deoxyxylulose-5-phosphate reductoisomerase).
                                                                                                                               -RILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                   43109 MW;
                                                                                                                                                                                                                                                                                                                                                                                             52.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TO THE DXR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                              57;
                                                                                                                                                                                                                                                                                                                                                                            Score 1047; DE
Pred. No. 1e-67
57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                   47D5B7A14E305BD0
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                                                                                                                                                                                                                                                                                                                                                                                                1047; DB 1;
No. 1e-67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   401
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) to 2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                            100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proteome
                                                                                                                                                                                                                                                                                                                                                                                                                 401;
                                                                                                                                                              -----QQVQTNLG
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RESERVATE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=K12 / W3110;
Takemoto K., Mori H., Murayama N., Kataoka K., Yano M., Itob T., Yamamoto Y., Inokuchi H., Miki T., Hatada B., Pukuda R., Ichiha Mizuno T., Makino K., Nakata A., Yura T., Sampei G., Mizobuchi "Systematic sequencing of the Escherichia coli genome: analysis "Systematic sequencing of the Escherichia coli genome: analysis "A.O - 6.0 min (189,987 - 281,416bp) region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

STRALN=K12 / Mc1655;

WEDLINE=997426617, PubMed=9278503;

Hattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Blattner F.R., Plunkett G. III, Bloch C.A., Rode C.K., Mayhew Riley M., Collado-Vides J., Glasner J. Conden M.A. Rose Riley M. Conden M.A. Rose
                                                                                                                                                                     MEDIINE=93077430; PubMed=1447125; Yamanaka K., Ogura T., Niki H., Hiraga S.; 'Identification and characterization of the of the mukB null mutant of Escherichia coll. J. Bacteriol. 174:7517-7526(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gregor J., Davis N.W., Kirkpatrick H.A., Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE=98374274; PubMed=9707569;
Takahashi S., Kuzuyama T., Watanabe H., Seto H.;
"A 1-deoxy-D-xylulose 5-phosphate reductoisomerase (
formation of 2-C-methyl-D-crythricol 4-phosphate in
nonmevalonate pathway for terpenoid biosynthesis.",
proc. Natl. Acad. Sci. U.S.A. 95:9879-9884(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-SSP-2003 (Rel. 42, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,
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Lashkari D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., STRAIN=K12 / W3110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia
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"Detection of new genes in three gene classes.";
                                                 Danchin
                                                                                                                                                                                                                                                                                                                                               Submitted
                                                                                                                                                                                                                                                                                                                                                                      Davis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science
                                                                        Barodovsky M.,
                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-49 FROM
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                                                                                                  MEDLINE=96032851;
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                                                                                                                                                                                                                                                                                                                                                                                        S., Duncan M., Allen B., Ara
., Federspiel N., Hyman R., I
i D., Lew H., Lin D., Namath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nplete genome sequence of 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P77209;
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                                                                                                                                                                                                                                                                                                                                               (SEP-1996)
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                                                                             McIninch
                                                                                                  PubMed=7567469
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                                                                                                                                                                                                                                                                                                 N.A.
                                                                          <u>د</u>ز
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                              മ
                                                                             Koonin
                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                              bacterial
                                                                                                                                                                                                                                                                                                                                                                                      Araujo R., Aparicio
., Kalman S., Komp C.
ath A., Oefner P., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli
                                                                          E.V.,
                              genome
                                                                             Rudd
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                            using Markov models
                                                                             Κ.E.,
                                                                                                                                                                                                                                                                                                                                                  databases
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                                                                                                                                                                                                                           gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  K-12.";
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n an alternative
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                                                                             Medigue
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yhew G.F.,
                                                                                                                                                                                                                           suppressor
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Matches 219
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CHARACTERIZATION, AND MUTAGENESIS.
MEDLINE=20347905; PubMed=10787409;
KUZNYAMA T., Takahashi S., Takagi M., Seto H.;
KUZNYAMA T., Takahashi S., Takagi M., Seto H.;
"Characterization of 1-deoxy-D-xylulose 5-phosphate reductoisomerase,
an enzyme involved in isopentenyl diphosphate biosynthesis, and
identification of its catalytic amino acid residues.";
J. Biol. Chem. 275:19928-19932(2000).
-1- FUNCTION: Catalyzes the NADP-dependent rearrangement and reduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                        MUTAGEN
MUTAGEN
MUTAGEN
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Radykewicz T., Rohdich F., Wungsintaweekul J., Herz S., Kis K.,
Eisenreich W., Bacher A., Zenk M.H., Arigoni D.;
"Biosyntheeis of terpenoids: 1-deoxy-D-xylulose-5-phosphate
reductoisomerase from Escherichia coli is a class B dehydrogenase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic
[7]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                ЧP
                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEBS
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MEDLINE=20123893; PubMed=10631325;
                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00183; -; 1.
InterPro; IPR003821; DXP_
                                                                                                                                                                                                                                                                                                                                                                                   EcoGene;
                                                                                                                                                                                                                                                                                BIND
                                                                                                                                                                                                                                                                                                                                                                                   , E64741; E52.
184741; E52.
1844; 27-FEB-02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrito 4-phosphate (MEP).
4-phosphate (MEP).
CARLYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+) = 1-deoxy-D-xylulose 5-phosphate + NADPH.
COPACTOR: REQUIRES A DIVALENT CATION; MAGNESIUM, MANGANESE OR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: Homotetramer.
SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : TINDEDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ENZYME REGULATION: INHIBITED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lett. 465:157-160(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                            D83536; BAA77848.1; -. U70214; AAB08602.1; -. D13334; -; NOT_ANNOTATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AE000126;
                                                                                                                  al Similarity
219; Conser
                                                                                                                                                                                                                                                                                                                       PF02670; DXP reductoisom; Ms; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AB013300; BAA32426.1; -.
13
                          61
                                                                                                                                                                                                                                                                                            Complete
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S-AKLLKTMLQQQGSRTEVLSGQQAACDMAALEDVDQVMAAIVGAAGLLPTLAAIRAGKT
                    KVASFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT
                                                                        MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
                                                          MKQLTILGSTGSIGCSTLDVVRHNPEHFRVVALVAGKNVTRMVEQCLEFSPRYAVMDDEA
                                                                                                                                                                             153
209
231
231
257
277
                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nonmevalonate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC73284.1; -.
                                                                                                                                                                                                                                                                                            proteome;
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14
153
209
231
231
284
                                                                                                                                                                              43388
                                                                                                                                 54.9%;
                                                                                                                                                                                                                                                                                                            Oxidoreductase; NADP; Magnesium;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE DXR FAMILY.
                                                                                                                  Score 1045; D
Pred. No. 1.4e
56; Mismatches
                                                                                                                    56
                                                                                                                                                                         NADPH (POTENTIAL).

G-D: DECREASE IN ACTIVITY.

H-QC: INCREASE IN YM.

H-QC: INCREASE IN YM.

E-K: DECREASE IN ACTIVITY.

H-QC: INCREASE IN YM.

RTPIAHTM -> VRQLPTPW (IN REF. 3

RTPIAHTM -> VRQLPTPW (IN REF. 3)
                                                                                                                                                                                                                                                                                                3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   terpenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY FOSMIDOMYCIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biosynthesis
                                                                                                                                 DB 1;
.4e-67;
                                                                                                                    118;
                                                                                                                                             Length 398;
                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathway;
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ETAIN-0157:H7 / RIMD 0509952;
EDLINE-21156231; PubMed-11256796;
EDLINE-21156231; PubMed-11256796;
In C.-G., Ohtsubo E., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
In C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
Inda T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
Inhara S., Shiba T., Hattori M., Shinagawa H.;
Iomplete genome sequence of enterohemorrhagic Escherichia coli
Complete genomic comparison with a laboratory strain K-12.";
IA Res. 8:11-22(2001).
I. FUNCTION. Catalyzes the NADP-dependent rearrangement and reduction
of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythritol
4-phosphate (MEP) (By similarity).
I. CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
E. 1-deoxy-D-xylulose 5-phosphate + NADPH.
E. 1-deoxy-D-xylulose 5-phosphate + NADPH.
E. PATHMAY: Nonmevalonate terpenoid biosynthesis pathway; second
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757
CR_ECO57
3-FEB-2003
9-FEB-2003
is SWISS-PROT entry is copyright. It is produced through a collaboration stween the Swiss Institute of Bioinformatics and the EMBL outstation - BEUTOPEAN Bioinformatics Institute. There are no restrictions on its se by non-profit institutions as long as its content is in no way addited and this statement is not removed. Usage by and for commercial ntities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prna N.T., Plunkett G. III. Burland V., Mau B., Glasner J.D., 1986 D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A., 1981 G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., 20tbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K., 20daca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., 1900 R.A., Blattner F.R.;
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EDLINE=21074935; PubMed=11206551;
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TRAIN=0157:H7 / E
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-ductoisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase)
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409:529-533(2001).
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(Rel. 41, Last annotation update)
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Best Local
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (DXP 1-deoxy-D-xylulose 5-phosphate reductoisomerase).
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Pfam; PF02670; DXP_reductoisom; 1.
TIGRFAMs; TIGR00243; Dxr; 1.
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PIR; G90650; G90650.
                    SEQUENCE PROM N.A.
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Isoprene biosynthesis; Oxidoreductase; NADP; Complete proteome.
NP BIND 7 14 NADPH (POTENTIAL).
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1.7e-67;
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InterPro; IPR003821; [
Pfam; PF02670; DXP_red
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-!- SIMILARITY: BELONGS TO THE DXR FAMILY.
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                              SEQUENCE FROM N.A.
STRAIN=MC58 / Serogroup B;
MEDLINE=20175755; PubMed=10710307;
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Relson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E.B.,
Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,
Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
"Complete genome sequence of Neisseria meningitidis serogroup B strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TIGR; NMB0184; -.
HAMAP; MF_00183; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AE002375; AAF40641.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (sogrene biosynthesis; Oxidoreductase; NADP; Complete
NP_BIND 9 16 NADPH (POTENTIAL).
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Ms; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         215;
                                                                                                                                                                                                                                                                                                                                                                                                                      66 RLEALLKRDGTÁ-TQVLHGAQÁLVDVÁSADEVSGVMCÁÍVGÁVGLPSALÁÁÁQKGKTIYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                  VVIHPQSIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGHMDF
                                                                                                                                                                                                                                                                       GPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNMEPDQIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTVLL 123
                                                                                                                      EKPELKRFPCIRLAYEAIKSGGIMPTVINAANEIAVEAFINEEVKFTDIAVIIERSMAQF
                                                                                                                                                                                                                                                                                                                                 ANKETLVVSGALFMETARANGAAVLPVDSEHNAVFQVLPRDYAGRLNEHGIASIILTASG
                                                                                                                                                                                                                                                                                                                                                                           ANKEAL VMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRILLTASG
FSDGIGDIGGLLAQDARTRAQARAFIGTL
                                     KPDDAGSLELVLQADQDAREVARDIIKTL 392
                                                                           VVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAYCLGLPERIDSGVGDLDFDALSALTF
                                                                                                                                                                                                                                                 GPFLTADIANT FOR IT PAQAVKH PNWRMGRKI SVDSATMMNKGLELI EAHWLFNCPPDKLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 1040.5; D
Pred. No. 3e-67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         126;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 394;
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RESULT 10 DXR_SALTY

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AMAP; MF 00183; -; 1.
nterPro; TPR003821; DXP_redisomrase.
Fam; PF02670; DXP_reductoisom; 1.
rrapaMs; TIGR00243; Dxr; 1.
rrapaMs; Tigr00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EDLINE=21534948; PubMed=11677609; (EDLINE=21534948; PubMed=11677609; (ICClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latre ourtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., L. eonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvan yan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M., Saterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      XR_SALTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
8-FEB-2003 (Rel. 41, Last sequence update)
9-FEB-2003 (Rel. 41, Last annotation update)
-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267) (DXP eductoisomerase) (1-deoxyxylulose-5-phosphate reductoisomerase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lature 413:852-856(2001).
i    FUNCTION: Catalyzes the NADP-dependent rearrangement and reductio
i    FUNCTION: Catalyzes the NADP-dependent rearrangement and reductio
i    for 1-decoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrito
4-phosphate (MEP) (By similarity).
i    CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
= 1-deoxy-D-xylulose 5-phosphate + NADPH.
i    PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              se by non-profit institutions as long as its content is in no way odified and this statement is not removed. Usage by and for commercial intities requires a license agreement (See http://www.isb-sib.ch/announce/r send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             his SWISS-PROT entry is copyright. It is produced through a collaboration etween the Swiss Institute of Bioinformatics and the EMBL outstation he European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 soprene biosynthesis; Oxidoreductase; NADP; Complete proteome
;P_BIND 7 14 NADPH (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CBI_TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nterobacteriaceae; Salmonella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acteria; Protechacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :- SIMILARITY: BELONGS TO THE DXR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Complete genome sequence of Salmonella enterica serovar Typhimurium
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                                    231
                                                                                                                                                                                                                                                                                   121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                            VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMP-----AGYTP----GHT
ACLLFNMEPDQIEVVIHEQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGV
                                                                                                                                                                                                                                                                                                                                                                                     KVAEFKQRIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
                                                                                               S----ILLIGSGGPFRETPMCDLAAMTPDQACRHPNWSMGRKISVDSATMMNKGLEYIE
                                                                                                                                                   AKQARRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATWWNKGLELIE
                                                                                                                                                                                                                           ILLANKESLYTCGRLFMDEVKRSNARLLPVDSEHNAIFQSLPQSIQHNLGYADLEQNGVF
                                                                                                                                                                                                                                                                                                                                           SAEQLKIMIQQHG-SRTEVLSGQQAACEMAALDEVGHVWAAIVGAAGLLPTLAAIRAGKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MKQLTILGSTGSIGCSTLDVVRHNPDSFRVIALVAGKNVARWAEQCLEFSPRVAVMDDTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43352 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1034; DB 1;
Pred. No. 8.8e-67;
8; Mismatches 105;
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N., Mulvaney E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0829As; 0829As; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 1-deoxy-D-xylulose 5-phosphate reductoisomerase (1-deoxyxylulose-5-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DXR SAL'
Q8Z9A6;
                                                                                                                                                                                                                                                                                                                                                       J. Bacteriol. 185:2330-2337(2003).

-i- FUNCTION: Catalyzes the NADP-dependent rearrangement and reduction of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrito 4-phosphate (MEP) (By similarity).

-i- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N...
SEQUENCE FROM N...
STRAIN=TY2 / ATCC 700931;
STRAIN=TY2 / ATCC 700931;
MEDLINE=22551367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Deng W., Liou S.-R., Plunkett G. C., Blattner F.R.;
RHTland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RHTland V., Kodoyianni V., Schwartz D.C., Blattner Typhi st
                                                    EMBL; AL627266; CAD08678.1; -.
EMBL; AE016834; AA067951.1; -.
HAMAP; MF 00183; -; 1
InterPro; IPR003821; DXP_redis
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enterobacteriaceae; Salmonella
   TIGRFAMs; TIGR00243; D:
Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete genome sequence of a enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SALTI
                                                                                                                                                                                                                                                                                       SIMILARITY:
                                                                                                                                                                                                                                                                                                                       PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     355
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                  PF02670; DXP reductoisom; Ms; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                       1-deoxy-D-xylulose 5-phosphate
NTHWAY: Nonmevalonate terpenoid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIA----VIIERSMAQFKPDDAGSLELVLQADQDAREVAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                       BELONGS TO THE DXR FAMILY
                                                        DXP_redisomrase
     Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a multiple drug resistant Salmonella
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biosynthesis
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       NADP;
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) to 2-C-methyl-D-erythritol
       Complete
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       proteome.
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                                                                                                                                           MEDLINE=20406833; PubMed=10953301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.I.
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Oin H., Dragoi I., Seller
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J
Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                        Q9KPV8;
16-OCT-2001
16-OCT-2001
28-FEB-2003
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                                                                                  Nature 406:477-483 (2000)

-i- FUNCTION: Catalyzes the NADP-dependent:
-i- FUNCTION: Catalyzes the NADP-dependent:
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                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=El Tor N16961
                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                   DXR OR
                                                                                                                                                                                                                                                                                                                                                                                                                         DXR_VIBCH
                                                                                                                        cholerae
                                                                                                                                                                                                                                                                                  NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                         OXR OR VC2254.
Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                  reductoisomerase)
                                                                                                                                 "DNA sequence of
                                                                                                                                                                                                                                                                                                                                                          -deoxy-D-xylulose
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           step.
SIMILARITY: BELONGS TO THE DXR FAMILY.
                                                           of 1-deoxy-D-xylulose-5-phosphate (EXP) to 4-phosphate (MEP) (By similarity). CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol
                                   PATHWAY:
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                                                 1-deoxy-D-xylulose 5-phosphate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MXGICII:GATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
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(Rel. 40,
(Rel. 41,
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                                     Nonmevalonate
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                                                                                                                                    poth
                                                                                                                                                                                                                                                                                                                                           40, Last sequence update)
41, Last annotation update)
61-phosphate reductoisomerase (EC 1.1.1.267)
61-deoxyxylulose-5-phosphate reductoisomerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14 N
43328 MW;
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                                                                                                                                     chromosomes
                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                     terpenoid
                                                                                                                                                                                                                                                                                                                                                                                    sequence
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Pred.
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No. 2.8e-66;
                                                                                                                                    of
                                                                                                                                     the
                                  + NADrn.
biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                           402
                                                                                                                                    cholera pathogen Vibrio
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                                                                                    rearrangement and reduction to 2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                    reductoisomerase).
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                                                             4-phosphate
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                                      pathway;
                                                                                                                                                                                                                            Gwinn M.L.,
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Best Local
                                                                                                                QRZH62;
QRZH62;
28-FBB-2003 (Rel. 41, Createu,
28-FBB-2003 (Rel. 41, Last sequence update,
28-FBB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWI
between
the Euro
STRAIN=CO-92 / Biovar Orientalis;
MEDLINB=21470413; PubMed=11586380;
Parkhill J., Wren B.W.; Thomson N.R., T
Prentice M.B., Sebaihia M., James K.D.,
Baker S., Basham D., Bentley S.D., Broo
                                                                                                       Yersinia pestis.
Bacteria; Proteobacteria;
Enterobacteriaceae; Yersin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AE004297; AAF9
PIR; D82099; D82099.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isoprene biosynthesis; Oxidoreductase; NADP; Complete
NP_BIND 7 14 NADPH (POTENTIAL).
SEQUENCE 402 AA; 43684 MW; 725DFF0BCDC27CB6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tigk; VC2254; -.
HAMAP; MF_00183; -; 1.
InterPro; IPR003821; DXP_
                                                                   SEQUENCE FROM N.A.
                                                                                            NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is SWISS-PROT entry is copyright. It is produced through a collaboration treen the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its e buropean Bioinformatics as long as its content is in no way dified and this statement is not removed. Usage by and for commercial titles requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                  FTDIALINDQVLSKVCATNTQLHCRDLESLLELDTMARHFAHQVLK
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                                                                                                                                                                                                                                                STANDARD;
                                                                                                           Yersinia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51.5%;
52.7%;
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Pred. No. 5.5e-66;
                                                                                                                                                                                                                                                PRT;
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  Brooks
                                                                                                                                                                                                                                                398
               Titball R.W., Holden M., Churcher C., Mungall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
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                                                                                                                                                               e (EC 1.1.1.267) reductoisomerase)
                                                                                                                          Enterobacteriales;
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                 ж <del>і</del>н
            <u>ا</u> ن
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TRAIN-KIN5 / Biovar Mediaevalis;

ZDLINB-22137863; PubMed-12142430;

zng W., Burland V., Plunkett G. III, Boutin A., May zng N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.

etherston J.D., Lindler L.E., Brubaker R.R., Plano craley S.C., McDonough K.A., Nilles M.L., Matson J.J.

zerry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nis SWISS-PROT entry is copyright. It is produced through stween the Swiss Institute of Bioinformatics and the Entre Buropean Bioinformatics Institute. There are no restrict by non-profit institutions as long as its content additional this statement is not removed. Usage by any
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Penome sequence of Yersinia pestis KIM.";
Bacteriol. 184:4601-4611(2002).
Bacteriol. 184:472es the NADP-dependent rearrangement and of 1-deoxy-D-xylulose-9-phosphate (DXP) to 2-C-methyl-D-4-phosphate (MEP) (By similarity).
1-CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate 1-deoxy-D-xylulose 5-phosphate + NADPH.
1-PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., eltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., eather S., Moule S., Oyston P.C.F., Quail M., Rutherford K., immonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; Genome sequence of Yersinia pestis, the causative agent of plagiture 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GRFAMs; TIGR00243; Dxr; 1.
soprene biosynthesis; Oxidoreductase; NADP;
P_BIND 7 14 NADPH (POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :am;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AMAP; MF_00183; -; 1.
nterPro; IPR003821; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                             EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AG0128; AG0128.
                                                                                                                                                                                              120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ414146; CAC89890.1; -. AE013914; AAM86681.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an email to license@isb-sib.ch).
                                                                                                                                                                                                                   VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMP-----AGYTPGHTAKQA
FCKVGALTPTTPDYQRYPCLKLAIDACNAGQAATTALNAANEISVMAFLDSKIRFTDIEV
                             I FEVGHMDFEKPDLKRFPCLRLAYEAI KSGGIMPTVLNAANEI AVBAFLNBBVKFTDIAV
                                                                                FWMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPBRFDSGVAPLD
                                                                                                                               SRIILTGSGGP
                                                                                                                                                      RRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLL
                                                                                                                                                                                              VILLANKESLITCGKLFMDEVKRSRAQLLFIDSEHNAIFQSLFERIQRQLGYS-SLNENGV
                                                                                                                                                                                                                                                               S-AKSLRILLAEQGSDTEVYSGETAACELAALDDVDQVMAAIVGIAGLPSTLAAIRAGKQ
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                                                                                                                                                                                                                                                                                                                              MKQLTILGSTGSIGNSTLSVVRANPELFKVTALVAGRNVREMAQQCLEFSPRYAAMSDEH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              requires a license agreement
                                                              FNASAEQIEVVLHPQSVIHSMVRYHDGSILAQMGTPDMRTPIAHAMAYPMRVSSGVAPLD
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2670; DXP_reductoisom; 1.
TIGR00243; DXr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             398 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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55.0%;
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                                                                                                                                                                                                                                                                                                                                                                                           Score 1020; DB
Pred. No. 8.8e-
51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NADPH (POTENTIAL)
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(See http://www.isb-sib.
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es 120;
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D.C.,
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[-D-erythritol
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P.
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355

IIERSMAQFKPDDAGSLELVLQADQDAREVARDIIKTL

392

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RESULT TO SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF SERVICE OF S
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P44055;
01-NOV-1995
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Pields C.A., Gozayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
08-FEB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductoisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Science 269:496-512(1995).

-i - FUNCTION: Catalyzes the NADP-dependent rearrangement and reduction of 1-decoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythritol 4-Phosphate (MEP) (By similarity).

-i- CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-Phosphate + NADP(+)

= 1-deoxy-D-xylulose 5-phosphate + NADPH.

-i- PATHWAY: Normevalonate terpenoid biosynthesis pathway; second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U32763; AAC22466.1; -. PIR; A64014; A64014.
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Pasteurellaceae; Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DXR OR HI0807
                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TIGR; H10807; -.
HAMAP; MF_00183; -; 1.
InterPro; IPR003821; DXP_redisomrase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                   Isoprene
NP BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Whole-genome random sequencing and
                                                                                                                                                                                                                                             Foca L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE DXR FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                      PF02670; DXP_reductoisom; 1.
AMS; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HI0807
                                  62
                                                                                        4.
                                                                                                                                              N
                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                VABEKQRIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTV 121
                                                                                           QNÍVÍLGSTGSÍGKSTLSVIENNÞQKYHAFALVGGKNVEAMFEQCIKFRÞHFAALDDVNÁ
                                                                                                                                                 KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK 61
                                                                                                                                                                                                                                                                                                                                   397 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KW20 /
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCC 51907;
                                                                                                                                                                                                                                                                                                                                   43667 MW;
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50.6%;
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=
                                                                                                                                                                                                              Score 1007; DB 1;
Pred. No. 7.5e-65;
6; Mismatches 111;
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                                                                                                                                                                                                                                                                                                                                   A6E9B24CC6A1CEAA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397
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                                                                                                                                                                                                                 111;
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                                                                                                                                                                                                                                                                          Length 397;
                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lee H.J., Kang H.S.;
Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the NADP-dependent rearrangement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND CHARACTERIZATION STRAIN-ATCC 31821 / ZM4 / CP4; MEDLINE-20461176; PubMed-11004410;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=ATCC 31821 /
                                                                                                                                                                                                                                                                                                                                                                                                                     -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Isolation of the dxr gene of Zymomonas mobilis and characterization of the 1-deoxy-D-xylulose 5-phosphate reductoisomerase."; FEMS Microbiol. Lett. 191:131-137(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grolle S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zymomonas mobilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DXR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
1-deoxy-D-xylulose 5-phosphate reductisomerase
reductoisomerase) (1-deoxyxylulose-5-phosphate r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29X5F2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 1-deoxy-D-xylulose-5-phosphate (DXP) to 2-C-methyl-D-erythrito 4-phosphate (MEP).

CATALYTIC ACTIVITY: 2-C-methyl-D-erythritol 4-phosphate + NADP(+)
                                                                                                                                                                                                                                                                    SIMILARITY:
                                                                                                                                                                                                                                                                                            SUBUNIT:
                                                                                                                                                                                                                                                                                                                                            PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                      ENZYME REGULATION: INHIBITED BY FOSMIDOMYCIN.
                                                                                                                                                                                                                                                                                                                                                                                                                     COFACTOR: REQUIRES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242
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AJ250714;
AF124757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122
                                                                                                                                                                                                                                                                                                                                                                                                                     1-deoxy-D-xylulose 5-phosphate + NADPH.
OFACTOR: REQUIRES A DIVALENT CATION; MAGNESIUM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64
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InterPro; IPR003821; DXP_redisomrase.
Pfam; PF02670; DXP_reductoisom; 1.
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Isoprene biosynthesis; Oxidoreductase; NADP; Magnesium; Manganese; Cobalt.
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CONFLICT 226 226 F -> Y (IN REF. 2).
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123 ANKESLVSAGGLMIDAVREHGTTLLPVDSEHNAIFQCF-----PHHNRDYVRRIIITASG 177
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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1: sp_archea:*
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
SUMMARIES
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No.	Score	1 3 2	1	BB	ID	Description
ب	1062	53.5	402	16	QBDBF5	Q8dbf5
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6	827.5	41.7	473	10	Q8L6C5	Q816c5
7	818.5	41.2	397	16	Q8D2G6	<u> </u>
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9	810.5	40.8	473	10	Q8W250	Q8 ₩250
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gar
Alteromonadaceae; Shewanella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-MR-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22297686; PubMed=12368813;
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NMEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERPDSGVAPLDI
                                                                                                                                      RILLTASGGPFRRTPIBTLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLF
                                                                                                                                                                                                                                                            VILANKEALVMSGQIFMQAVSDSGAVILIPIDSEHNAIFQCMPAGYTPG-----HTAKQAR 175
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                                                                                             HILLTGSGGPFLTAELSNLAAMTPAQACKHPNWSMGPKISVDSATMMNKGLEFIBARWLF
                                                                                                                                                                                                                                                                                                                                 AALALKAQLPAA--LNIQVTSGEDELIALVTAPAVDTVMAAIVGAAGLVPTLAAVKAGKR
                                                                                                                                                                                                                                                                                                                                                                KVAEFKORIAASPVADIKVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                        KOMMVILGATGSIGASTLSVISANPTAYRVYALVANASVDKMLTLCLAHRPOVAHNVDHK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYBQCLAHHPEYAVVVMES
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                                                                                                                                                                                                                 VILLANKEAL VMSGELFIBATRASGATILIPVISEHNAI FQCLPBEVQSNLGRCDLAASGIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. 396 AA; 42159 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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(TIEMBLIFE1. 23, Last sequence update)
(TIEMBLIFE1. 23, Last annotation update)
ylulose 5-phosphate reductoisomerase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52.5%; Score 1041.5; DB 16; Length 396; 55.1%; Pred. No. 2.3e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gammaproteobacteria; Alteromonadales;
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MA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

Deboy R., Gwinn M.L., Nelson W.C., Haft D.H.,

Deboy R.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

Hartickey B.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

Hartickey B.K., Peterson J.D., Durkin A.S., Kolonay J.L., Parksey D.,

Hartickey B.K., Peterson J.D., Brenner M., Shea T.F., Parksey D.,

Hartickey B.K., Peterson J.D., Hansen C.L., Craven M.B., Radune D.,

Vamathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

Hartickey B.K., Peterson B. Bryant D.A., Fraser C.M.;

"The complete genome sequence of Chlorobium tepidum TLS, a

"Thotosynthetic, anaevobic, green-sulfur bacterium.";

Depot. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
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Pfam; PF02670; DXP_reductoisom; 1.
TIGREAMs; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AB012791; AAM71373.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chlorobium tepidum.
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01-MAR-2003
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11-OCT-2002 (TrEMBLrel. 22, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
-deoxy-D-xylulose 5-phosphate reductoisomerase.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                       GHMDFEKPDLKRFPCLRLAYBAIKSGGIMPTVLNAANBIAYBAPLNBBVKFTDIAVIIER
                                                                                                                                                                   LTASGGPFRRTPIETLSSYTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFNME
                                                                                                                                                                                                                                KTVLLANKBALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQARRIL
                                                                                                                                                                                                                                                                         SRERLK-----GMLGDHKPEILCGLEGAAEVAAVDGADMVVSAIVGAAGLVPTVRAIEAG
                                                                                                                                                                                                                                                                                                                                                                   MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMES
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ATLTFEEPDMERFPALRLAFDALKAGQTYPAVLNAANEIAVAAFLDKKIGFTDIAGTVDK
                                                                AEKIGVVVHPQSIIHSMYEYIDGCVIAQUGVPDMRAP
                                                                             PDQIEVVIHPOSIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAMPERFDSGVAPLDIFEV
                                                                                                                                                                                                      KDIALANKETLVVAGQLVSDLVKKHDVKLLPVDSEHSAIFQSL-----VGHRTEDIERII
                                                                                                                                                                                                                                                                                                           KVAEFKORIAASPVADIK--VLSGSEALOQVATLENVDTVMAAIVGAAGLLPTLAAAKAG
                                                                                                                                                                                                                                                                                                                                             MKSLSILGSTGSIGLSTLDVVRRHPERFSIAALAEGHDVEMLLKQIDBFRPSLVSVRDEA
                                                                                                                                  NEDCLLSVPKQAMASIEDIIALDAQTRIYARELL 392
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                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                 49.5%; Score 983; DB 1 50.6%; Pred. No. 5e-65;
                                                                                                                                                                                                                                                                                                                                                                                                                 75; Mismatches
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Q9SP64 PRELIMINARY;
Q9SP64;
01-MAY-2000 (TrEMBLzel. 1
01-MAR-2001 (TrEMBLzel. 1
01-JUN-2002 (TrEMBLzel. 2
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura Y., Kaneko T., Sato S., İkeuchi M., Katoh H., Sasamot Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; "Complete genome structure of the thermophilic cyanobacterium Thermosynechococcus elongatus BP-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synechococcus elongatus (Thermosynechococcus elongatus). Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
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45.4%; Pred. No. 1.5e-56;
tive 76; Mismatches 123;
     13,
16,
21,
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     Last sequence update)
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rtemisia annua (Sweet wormwood).
ikaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
permatophyta; Magnoliophyta; eudicotyledons; core eudicots;
steridae; campamilids; Asterales; Asteraceae; Asteroideae;
nthemideae; Artemisia.
                                                                                                                                                                                                                                                                     3L6C5;
1-0CT-2002
1-0CT-2002
1-MAR-2003
                                                                                                                                          evia rebaudiana (Stevia).

karyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

permatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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| bbe K.K., Souret F.F., Shore K.A., Weathers P.
| \text{\text{tremisia annua 1-deoxy-D-xylulose-5-phosphate}
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                                                                                                                     steridae; campanulids;
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dBL; AF182287; AAD56391.2; ...
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OUENCE FROM N.A.
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JBI_TaxID=55670;
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(TrEMBLrel. 22,
(TrEMBLrel. 23,
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Pred. No. 3.9e-54;
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5-phosphate reductoisomerase
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EMBL, AJ429233, CAD22156.1,
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Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
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Pfam; PP02670; DXP reductoisom; 1.
TIGRFAMs; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                        flies, Wigglesworthia glossinidia.";
Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24534.1; -.
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                                                                                 Conservative
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                                                                                                                                                                             44663 MW;
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Last sequences
                                                                                 Score 818.5; DB 16;
Pred. No. 9.4e-53;
%1; Mismatches 130;
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Pred. No. 2.6e-53;
1; Mismatches 129;
                                                                                                                                                                               485355F55256BDF6 CRC64;
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MKGICILGATGSIGVSTLDVVARHPDKYQVVALTANG-NIDALYEQCLAHHPEYAVVVME 59

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ZMBL, AF331705, AAK96063.2; --
InterPro; IPRR003821; DXP redisomrase.
Pfam, PF02670; DXP reductoisom; 1.
TIGREPAMs; TIGR00243; Dxr; 1.
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MEDLINB=21425086; PubMed=11532167;

MEDLINB=21425086; PubMed=11532167;

Rodriguez-Concepcion M., Ahumada I., Diez-Juez B., Sauret-Gueto
Rodriguez-Concepcion M., Ahumada I., Diez-Juez B., Sauret-Gueto
Lois L.M., Gallego F., Carretero-Paulet L., Campos N., Boronat P
"1-Deoxy-D-xylulose 5-phosphate reductoisomerase and plastid
isoprenoid biosynthesis during tomato fruit ripening.";
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
1-deoxy-D-xylulose-5-phosphate reductoisomerase.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; lamiids; Solanales; Solanaceae; Solanum.
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                                                                                                                                                           VAEFKQRIAASPVADI----KVLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     YFTDIAIINKKVLDKLDIFEPSSIEEILLLDSKARNLAKKFIK 395
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GKDIALANKETLIAGGPFVLPPAHKHKVKILPADSEHSAIFQCIQGLPEG-
                                                   GKTVLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQC---MPAGYTPGHTAKQA
                                                                                                                VESTKDAL----ADMEDKPEIIPGEQGVIEVARHPDAVTVVTGIVGCAGLKPTVAAIEA
                                                                                                                                                                                                                           KPISIVGSTGSIGTQTLDIVAENPDKFRVVALAAGSNVTLLADQVKTFRPKLVAVRNESL
                                                                                                                                                                                                                                                             KGICILGATGSIGVSTLDVVARHÞDKYQVVALTANGNIDALYEQCLAHHÞEYAVVVMESK
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                                                                                                                                                                                                                                                                                                                                            69;
                                                                                                                                                                                                                                                                                                                                      Score 816.5; DB 1
Pred. No. 1.7e-52;
9; Mismatches 125
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Q8W250; Q1-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001) to the EMBL/GenBank/DDBJ EMBL; AF367205; AAL37560.1; -. Gramene; Q8W250; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR003821; DXP_redisomrase. Pfam; PF02670; DXP_reductoisom; 1. TIGRPAMs; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Carretero-Paulet L., Boronat A., Campos N.;
"1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR),
first committed step of the mevalonate-independent path
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1-deoxy-D-xylulose 5-phosphate reductoisomerase precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biosynthesis.";
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DIFEVGHYDFEKPDLKREPCLRLAYEAIKSGGIMETVLAVAANEIAVEAFLNESVKFTDIA
                                                AEYDDIBIVIHPOSIIHSMIETQDSSVLAQLGWPDMRIPILYTMSWPDRIYCSEVTWPRL
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                                                                                    MEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPER-FDSGVA--PL
                                                                                                                                         DIALANKETLIAGGPFVLPLAQKHKVKILPADSEHSAIFQCIQGLPEG-----ALRR
                                                                                                                                                                                                                                                  TVLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQC---MPAGYTPGHTAKQARR
                                                                                                                                                                                                                                                                                                   VDELKEALAD----CDWKPEIIPGEQGVIEVARHPDAVTVVTGIVGCAGLKPTVAAIEAGK
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                                                                                                                                                                               ILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLELIEACLLFN 236
                                                                                                                                                                                                                                                                                                                                       VAEFKQRIAASPVADIK--VLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGK 119
                                                                                                                                                                                                                                                                                                                                                                                                                   KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYBQCLAHHPEYAVVVMESK 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           473 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.8%; Score 810.5; DB J
45.4%; Pred. No. 4.8e-52;
tive 67; Mismatches 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             123;
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1-MAR-2001 (TEMBLrel. 16, Last sequence update)
1-OCT-2002 (TEMBLrel. 22, Last annotation updat-deoxy-d-xylulose-5-phosphate reductoisomerase. 0005A05.19 OR P0482C06.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQUENCE
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permatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
nrhartoideae; Oryzeae; Oryza.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ibmitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
dBL; AP002863; BAB16915.1; -.
dBL; AP002845; BAB78606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cne: P0482C06."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa nipponbare (GA3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRAIN=cv. Nipponbare;
saki T., Matsumoto T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           lone: P0005A05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QUENCE FROM N.A.
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                                                                                                                      306
                                          366
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    354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pro; IPR003821; DXP_redisomrase
PF02670; DXP_reductoisom; 1.
AMs; TIGR00243; Dxr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                  8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                              DIALANKETLIAGGPFVLPLAQKHKVKILPADSEHSAIFQCIQGLPEG-----ALRR
                                                                                                                                                                                                                                                                                                                                                                                              VAEFKQRIAASPVADIK--VLSGSEALQQVATLENVDTVMAAIVGAAGLLETLAAAKAGK 119
    VIIB---
                                          DLCKLGSLTFKAPDNVKYPSMDLAYAAGRAGGTMTGVLSAANEKAVELFIDEKIGYLDIF
                                                                              DIFEVGHMDFEKPDLKRFPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIA 353
                                                                                                                    ARYDDIETVIHPOSIIHSMIETQDSSVLAQLGWPDMRIPILYTMSWPDRIYCSEVTWPRL
                                                                                                                                               MEPDQIEVVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPER-FDSGVA--PL
                                                                                                                                                                                                    ILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDWGRKISVDSATWMNKGLELIEACLLFN 236
                                                                                                                                                                                                                                                                                                                    TVLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQC---MPAGYTPGHTAKQARR 176
                                                                                                                                                                                                                                                                                                                                                            VDELKEALAD----CDWKPEIIPGEQGVIEVARHPDAVTVVTGIVGCAGLKPTVAAIEAGK
                                                                                                                                                                                                                                                                                                                                                                                                                                          KPISIVGSTGSIGTQTLDIVAENPDKFRVVALAAGSNVTLLADQVKTFKFKLVAVRNBSL 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KGICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVVELTCDAHRNELVTRP---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DLCKLGSLTFKAPDNYKYPSMDLAYAAGRAGGTMTGVLSAANEKAVELFIDEKIGYLDIF 425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SEP-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      473 AA;
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    --RSMAQFKPDDAGSLELVLQADQDAREVARDI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RSMAQFKPDDAGSLELVLQADQDAREVARDI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40.7%; Score 807.5; DB 45.4%; Pred. No. 8e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51473 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66; Mismatches 124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       moto K.;
genomic DNA,
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genomic DNA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 1,
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RESULT 12
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AC Q9FXZ
AC Q9FXZ
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DT 01-MA
DT 01-MA
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ID Q9M4W
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AC Q9M4W
DT 01-OC
DT 01-OC
DT 01-OC
DT 01-U
DT 10-C
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CC Eukan
OC Sperr
CC Aster
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Best Local S
Matches 176
       Q9FXZ7;
01-MAR-2001
01-MAR-2001
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9M4W4;
01-OCT-2000 (TrEMBLrel: 15,
01-OCT-2000 (TrEMBLrel: 15,
01-JUN-2002 (TrEMBLrel: 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Veau B., Courtois M., Oudin A., Chenieux J.-C., Rideau "Cloning and expression of cDNAs encoding two enzymes pathway in Catharanthus roseus "; Biochim. Biophys. Acta 1517:159-163(2000).

EMBL; AF250235; AAF65154.1; -.
InterPro; IPR003821; DXP_redisomrase.
Pfam; PF02670; DXP_reductoisom; 1.
FIGRFAMs; TIGR00243; DXr; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Catharanthus roseus (Rosy periwinkle) (Madagascar periwinkle).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; lamiids; Gentianales; Apocynaceae; Rauvolfioideae; Vinceae;
                                                                                                       Q9FXZ7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isomerase.
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9M4W4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4058;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Catharanthus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VLLANKEALVMSGQIFMQAVSDSGAVLLPIDSEHNAIFQC---MPAGYTPGHTAKQARRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KPISIVGSTGSVGTQTLDIVAENPDKFRVVALAAGSNVTLLADQVKTFKPQLVSVRNESL
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                                                                                                                                                                                                                                  VVBLTCAKHQAELVTSPSLDEIIHYDLGARDYAASFQNSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EPDQIEVVIHBQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAP---LD
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                                                                                                                                                                                                                                                                               IIERSMAQFKPD--DAGSLELVLQADQDAREVARDIIKTL 392
                                                                                                                                                                                                                                                                                                                                    LCKLGSLTFKTFDNVKYFSMDLAYAAGRAGGTMTGVLSAANEKAVELFIDEKISYLDIFK
                                                                                                                                                                                                                                                                                                                                                            IPEVGHMDPEKPDLKREPCLRLAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                    EYDNIDIVIHPQSIIHSMVETQDSSVLAQLGWPDMRLPILYTLSWPDRISCSEITWPRLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILTASGGAFRDWFVEKLKEVKVADALKHPNWNWGKKITVDSATLFNKGLEVIEAHYLFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TALANKETLIAGXPFVLPLAHKHKVKILPADSEHSAIFQCIQGLPEG-----ALRRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNBLKE--ALSDVDDKPBIIPGBQGVVBVVRHSDAVTVVTGIVGCAGLKPTVAAIBAGKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 AA;
       (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                          PRELIMINARY,
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16,
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                             Created)
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 803.5; DB 10;
Pred. No. 1.6e-51;
1; Mismatches 134;
                                                                                                          PRT;
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"Regulation of the non-mevalonate methylerythritol phosp
pathway by mycorrhizal fungi.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ297566; CAC03581.1;

InterPro; IPR003821; DXP_redisomrase.

Pfam; pF02670; DXP_redisomrase.

Pfam; pF02670; DXP_redisomrase.

IIGRFAMS; TIGR00243; DXr; 1.
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1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC DXR OR LA3292.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poa
PACCAD clade; Panicoideae; Andropogoneae; Zea.
     Submitted (MAR-2002) to the EMBL/GenBank/DDBJ
SMBL; AE011490; AAN50490.1; -.
Isomerase; Oxidoreductase; Complete proteome.
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45.1%; Pred. No. 1.9e-51;
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01-MAY-1999
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                                                                                                                                                                                                                                                                                                                                         Altincicek B., Sanderbrand S., Wiesner J., Jomaa H.;
"dxr as a potential target for antimalarial drugs.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF111813; AAD03739.1; -...
EMBL; PF111813; AAD03739.1; -...
Pfam; PF026570; DXP reductoisom; 1.
TIGRPAMS; TIGRO0243; Dxr; 1.
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                                                                                                                             ICILGATGSIGVSTLDVVARHPDKYQVVALTANGNIDALYEQCLAHHPEYAVVVMESKVA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EKPOLKREPCLRIAYEAIKSGGIMPTVLNAANEIAVEAFLNEEVKFTDIAVIIERSMAQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVIHPQSIIHSMVDYVDGSVLAQMGNPDMRTPIAHAMAWPERFDSGVAPLDIFEVGHMDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANKEALVMSGQIFMQAVSDSGAVLLFIDSBHNAIFQCMPAGYTPGHTAKQARRILLTASG 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DV--GVLGNKLGRTQILYGESSLCELVREPEVEIVITAIVGSVGLRPTIAAITAGKRLGI
  GKTVLLANKEALVMSGQ1FMQAVS-DSGAVLLPIDSEHNA1FQCMPAGYTPGHTAKQ---
                                           SVYEELKELV -- KNIKDYKPIILCGDEGMKEICSSNSIDKIVIGIDSFQGLYSTMYAIMN 196
                                                                                    SKVAEFKORIAASPVADIK--VLSGSBALGOVATLENVDTVMAAIVGAAGLLFTLAAAKA
                                                                                                                                                                    ICILGATGSIGVSTLDVVARHPDK----YQVVALTANGNIDALYEQCLAHHPEYAVVVME 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KIEFPLSLEEYEEADRIARETVRML 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPDDAGSLELVLQADQDAREVARDI 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPOFKRYPGIGLAFEAGKVGGTAFCIFNAANEAAVELFIKDEIRFIBIPDYIRETLDEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VVIHPQSIAHGIVELKDGASFLYASYPDMIFPIAHSLFHPEPVPKVLRSYPAKDWGKLEF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EFKORIAASPVADIKVLSGSBALQQVATLENVDTVMAAIVGAAGLLPTLAAAKAGKTVLL 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391
                                                                                                                                                                                                                                                                                                       488 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBirel 10, Created)
(TrEMBirel 10, Last sequence update)
(TrEMBirel 21, Last annotation update)
ylulose 5-phosphate reductoisomerase.
                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                       55756 MW; 4E280C81CDFAD3EF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43026 MM;
                                                                                                                                                                                                             36.8%; Score 729.5; DB 5; Length 37.8%; Pred. No. 5.4e-46; tive 88; Mismatches 141; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.1%; Score 735.5; DB 16; Length 41.0%; Pred. No. 1.4e-46; tive 78; Mismatches 140; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Apicomplexa; Haemosporida; Plasmodium
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1-MAR-2003
1-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ture 419:498-511(2002)
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karyota; Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              L-MAR-2003 (TrEMBLrel. 23, Created)
L-MAR-2003 (TrEMBLrel. 23, Last seguence update)
L-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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                                                                                                                                                                                                                    SVYEELKELV--KNIKDYKPIILCGDEGMKEICSSNSIDKIVIGIDSFQGLYSTMYAIMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----ARRILLIASGGPFRRTPIETLSSYTPDQAVAHPKWDMGRKISVDSATMYNKGLEL
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                                             SKINNINKIFICSSGGPFONLTMDELKNVTSENALKHPKWKWGKKITIDSATWWNKGLEV
                                                                                                                                NKIVALANKESIVSAGFFLKKLLNIHKNAKIIPVDSBHSAIFQCLDNNKVLKTKCLQDNF
                                                                                                                                                                         GKTVLLANKEALVMSGQIFMQAVS-DSGAVLLPIDSEHNAIFQCMPAGYTPGHTAKQ----
                                                                                                                                                                                                                                                           SKVAEFKQRIAASPVADIK--VLSGSEALQQVATLENVDTVMAAIVGAAGLLPTLAAAKA 117
                                                                                                                                                                                                                                                                                                         VAIFGSTGSIGTNALNII-RECNKIENVFNVKALYVNKSVNELYEQAREFLPEYLCIHDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              488
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                                                                           --ARRILLTASGGPFRRTPIETLSSVTPDQAVAHPKWDMGRKISVDSATMMNKGLEL
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                                                                                                                                                                                                                                                                                                                                                                                                              36.8%; Score 729.5; DB 5; 37.8%; Pred. No. 5.4e-46;
                                                                                                                                                                                                                                                                                                                                                                                         88;
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Plasmodium

7

483

376

288 316 228

Length Indels

488; 23;

Gaps

138 59

316

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TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 459 amino acids
TYPE: amino acid
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-309-026-2
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Search completed: January 29, 2004, 15:57:04
Job time : 8.2499 secs
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APPLICANT: Mooney, Jeffrey L.
APPLICANT: Debouck, Christine M.
APPLICANT: Zhong, Yi Yi
TITLE OF INVENTION: No. 6204042el GlmU
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSE: Dechert Price & Rhoads
STREET: 4000 Bell Atlantic Tower, 1717 Arch Stre
CITY: Philadelphia
STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.4%; Score 88.5; DB 3; Length 459; Best Local Similarity 23.9%; Pred. No. 0.12; Matches 48; Conservative 32; Mismatches 74; Indels 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: DICKINSON, Todd Q
REGISTRATION NUMBER: 28,354
REFERENCE/DOCKET NUMBER: GM10024
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-994-2252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 19103
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: BastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/309,026
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/971,782
PRIOR APPLICATION NUMBER: 08/971,782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 215-994-2222
                                                                                             148 EVLRMVEQKDATDFEKQIKBI 168
                                                                                                                                            177 DALORTEGNPAVTDEASALEL 197
                                                                                                                                                                                                                               125 DTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQM----FKYGML-----R 176
                                                                                                                                                                                      99 -----IAGDTPLITGESLKNL----IDFHINHKNVATILTAETDNPFGYGRIVRNDNA 147
                                                                                                                                                                                                                                                                                                                                68 SIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDA---ARPCLTGSDIHLQI 124
                                                                                                                                                                                                                                                                                         47 -----KTVTVVGHK--ASIVEEVLAGQTEFVTQSEQLGTGHAVMMTEPILEGISGHTLV 98
                                                                                                                                                                                                                                                                                                                                                                                    8 WAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTL/TRLLESDAFQKVAVAISVEDPYWPEL 67
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Minimum
Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgm2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgm2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

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11: /cgm2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

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US-09-934-868-68
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Sequence 6, Appli
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Sequence 11722, A
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ALIGNMENTS

Que / Match 100.0%; Score 1199; DB 10; Length 231; Bes! Local Similarity 100.0%; Pred. No. 2.1e-115; Matches 231; Conservative 0; Mismatches 0; Indels 0; Gaps 0 Qy MNPTIQCWAVVPAAGVGKMADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE 60 Db MNPTIQCWAVVPAAGVGKMADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE 60 Ov 61 NDVWDRISTAKHPDITTARGGKERANGVISALKALRDIASENDWYLVHDAARPCLTGSDI 120
100.0%; Score 1199; DB 10; Length 231;
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PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 81
SOFTWARE: Microsoft Office 97
SEQ ID NO 68
LENGTH: 231
TYPE: PRT
TYPE: PRT
TOGRANISM: Methylomonas 16a
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                                                                                                                                                                                                                                           Sequence 10, Application US/09941947A Publication No. US20030003528A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Amino acid sequences encoded by ISPD -09-934-868-68
APPLICANT: Picataggio, Steve APPLICANT: Rouvière, Pierre E. TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE FILE REFERENCE: CL1903 US NA CURRENT APPLICATION NUMBER: US/09/941,947A
                                                                                                                                                                             APPLICANT: Brzostowicz, Patricia C.
APPLICANT: Cheng, Qiong
APPLICANT: DiCosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/934,868
CURRENT FILING DATE: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Odom, James M
APPLICANT: Schenzle, Andreas J
TITLE OF INVENTION: DENTRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1596 US NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOffas, Mattheos
APPLICANT: Odom, James M
APPLICANT: Schenzle, Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
es 231; Conserv
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US20020137190A1
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DiCosimo, Deana J.
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                                                                                                                                Miller, Edward S. Jr
                                                                                                                                                                                                                                                                                                                                                                                                        RTEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
                                                                                                           Odom, J. Martin
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E FOR APPLICATION NUMBER: 60/229,907
E DIOR FILING DATE: 2000-09-01
P DIOR APPLICATION NUMBER: 60/229,858
E LOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
S FTWARE: Microsoft Office 97
SED ID NO 10
SENGTH: 231
'YPE: PRT
RGANIEM: Methylomonas 16a
US-C -941-947A-10
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C REENT FILING DATE: 2001-03-21
LIOR APPLICATION NUMBER: 60/191,078
FIOR PILING DATE: 2000-03-21
FIOR APPLICATION NUMBER: 60/207,727
FIOR PILING DATE: 2000-05-23
FIOR PILING DATE: 2000-05-23
FIOR PILING DATE: 2000-05-26
FIOR PILING DATE: 2000-10-23
FIOR PILING DATE: 2000-10-23
FIOR APPLICATION NUMBER: 60/22,578
FIOR APPLICATION NUMBER: 60/253,625
FIOR APPLICATION NUMBER: 60/257,931
FIOR APPLICATION NUMBER: 60/257,931
FIOR APPLICATION NUMBER: 60/269,308
FIOR FILING DATE: 2000-11-27
FIOR APPLICATION NUMBER: 60/257,931
FIOR APPLICATION NUMBER: 60/269,308
FIOR FILING DATE: 2001-02-16
FIOR PILING DATE: 2001-02-16
FIOR PILING DATE: 2001-02-16
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A PLICANT:
A PLICANT:
E PLICANT:
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ኔ PLICANT: Ohlsen, Kari L.
ኔ PLICANT: Zyskind, Judith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLICANT: Xu, H. Howard
TLE OF INVENTION: Identification of Essential Genes
TLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          :::ence 11931, Application US/09815242
ent No. US20020061569A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LE REFERENCE: BLITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .3RAL INFORMATION:
RGANISM: Pseudomonas aeruginosa
-815-242-11931
                                                                                                                                                 MBER OF SEQ ID NOS:
                                                                          ENGTH: 234
                                                                                               ID NO 11931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 HLQIDTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 RTEGNPAVIDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DPYWPELSIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MNPTIQCWAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 100.0%; Score 1199; DB 11; Similarity 100.0%; Pred. No. 2.1e-115; 31; Conservative 0; Mismatches 0;
                                                                                                                       FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RTEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPYMPELSIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLIGSDI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MNPTIQCWAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HLQIDTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Carr, Grant J.
Yamamoto, Robert T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTMARE: PastSEQ for Windows Version 4.
SEQ ID NO 11076
LENGTH: 225
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US-09-815-242-11076
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                                                                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Haemophilus influenzae US-09-815-242-11076
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR PILING DATE: 2000-03-21
PRIOR PILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR PRICES DATE: 2000-10-23
PRIOR PRICES DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
PRIOR FILING DATE: 2000-10-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Haselbeck, Robert APPLICANT: Ohlsen, Kari L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Prokaryotes
                                                                                                                                                                                                                            Local Similarity
  67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVAITDEASAMEWAGYAPKLVEGRADNLKITTPEDLLRLQ 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKNDPVGGILALSSHDTLKHVDGD-TITATIDRKHVWRALTPQMFKYGMLRDAL-QRTEG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DCAASRHVQRAAGGAERAGSVINGLIRLIELGAQADDWVIVHDAARPNITRGDLDRLLEE
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L--DPKIQLVEGGTTRAESVLNGLNA---TAEKNAWVLVHDAARPCLQ----HADIDKIL 117
                             IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WTVIPAAGVGSRMRADRPKQYLDLAGRTVIERTLDCFLEHPMLRGLVVCLAEDDPYWPGL
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                                                                                                AVLPAAGVGSRMQADKPKQYLTLLGKTLLEHTLDVMLSYPAVSKIILAVSKDDPYISTLS
                                                                                                                                              AVVPAAGVGKRAQADRPXQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPBLS
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                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                 44.2%; Score 530.5; DB 9; 52.5%; Pred. No. 1.9e-46; tive 28; Mismatches 65;
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CURENT FILING DATE: 2001-03-21
PE OR APPLICATION NUMBER: 60/191,078
PE OR FILING DATE: 2000-03-21
PE OR APPLICATION NUMBER: 60/206,848
PE OR FILING DATE: 2000-05-23
PE OR APPLICATION NUMBER: 60/207,727
PE OR APPLICATION NUMBER: 60/242,578
PE OR FILING DATE: 2000-05-26
PE OR APPLICATION NUMBER: 60/242,578
PE OR RILING DATE: 2000-10-23
PE OR APPLICATION NUMBER: 60/253,625
PE OR APPLICATION NUMBER: 60/257,931
PE OR APPLICATION NUMBER: 60/257,931
PE OR APPLICATION NUMBER: 60/269,308
PE OR APPLICATION NUMBER: 60/269,308
PE OR APPLICATION NUMBER: 60/269,308
PE OR FILING DATE: 2001-02-16
PE OR FILING DATE: 201-02-16
PE OR FILING DATE: 2010-0
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LICANT: Ohlsen, Kari L
LICANT: Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CANISM: Klebsiella pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LICANT: Xu, H. Howard
LE OF INVENTION: Identification of Essential Genes
LE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                                                                                                                                                                                                                              / Match 44.2%; Score 529.5; DB 9;
Local Similarity 51.1%; Pred. No. 2.9e-46;
les 114; Conservative 30; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE: ELITRA.011A
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                                                                                                                                            129 NDPVGGILALSSHDTLKHVVG-GDT-ITATIORKHVWRALTPQMFKYGMLRDALQR--TEG
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                                                                                                                                                                                                                       93
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TSRVGGILAAPVROTMKRAEPGKTAIAHTVDRNDLWHALTPQLFPRELLVDCUTRALNEG
                                                                                                                                                                                                                       LAQHPQITVVDGGABRADSVLAGLQAL----PEAQWVLVHDAARPCLHQDDLSRLLSICE 148
                                                                                                                                                                                                                                                                                                                                AVVPAAGFGRRMQTECPKQYLSIGNKTILEHAVAALLADARVQRVVIAVSPGDRRFSQLP
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US-09-815-242-10273
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PRIOR PILLING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILLING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILLING DATE: 2000-05-26
PRIOR PILLING DATE: 2000-10-23
PRIOR PILLING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR APPLICATION NUMBER: 60/269,308
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US-09-792-251-11
GENERAL INFORMATION:

APPLICANT: Fritz, Christian

APPLICANT: Youngman, Philip

APPLICANT: Youngman, Luz-Maria

TITLE OF INVENTION: USE OF YACM AND YOEJ, ESSENTIAL BACTERIAL GENES AND FOLYPEPTIDES

TITLE OF INVENTION: AND THEIR USE

FILE REFERENCE: 06286-140001

CURRENT FILING DATE: 2001-02-23

CURRENT FILING DATE: 2001-02-23
                                                                                                                                                                                                                          Sequence 11, Application of the No. US20020160364A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 111;
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SEQ ID NO 10273
LENGTH: 236
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PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                               126 TSRTGGILAAPVRDIMKRAEPGKNAIAHTVDRNGLWHALTPOFFPRELLHDCLTRALNEG 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 NDPVGGILALSSHDTLKHVD--GDTITATIDRKHVWRALTPQMFKYGMLRDALQR--TEG 184
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Trawick, John D.
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Yamamoto, Robert T.
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                                                                                                                                                                                                                                                                         Application US/09792251
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20061569A1
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US-()-815-242-13867
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                                                                                                                                                                                                                                                                                                                 ICE REFERENCE: ELITRA.011A
CREENT PILLING DATE: 2001-03-21
LIOR APPLICATION NUMBER: 60/191,078
LIOR APPLICATION NUMBER: 60/191,078
LIOR APPLICATION NUMBER: 60/206,848
LIOR APPLICATION NUMBER: 60/207,727
LIOR APPLICATION NUMBER: 60/207,727
LIOR APPLICATION NUMBER: 60/207,727
LIOR FILLING DATE: 2000-05-23
LIOR APPLICATION NUMBER: 60/242,578
LIOR APPLICATION NUMBER: 60/242,578
LIOR APPLICATION NUMBER: 60/253,625
LIOR APPLICATION NUMBER: 60/253,625
LIOR APPLICATION NUMBER: 60/257,931
LIOR APPLICATION NUMBER: 60/257,931
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LIOR APPLICATION NUMBER: 60/257,931
LIOR FILING DATE: 2000-11-27
LIOR FILING DATE: 2001-02-16
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)RGANISM: Escherichia coli
)-792-251-11
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PLICANT: Xu, H. Howard
TLE OF INVENTION: Identification of Essential Genes
TLE OF INVENTION: Prokaryotes
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                                                                                                                                                                                                                      IMBER OF SEQ ID NOS: 14110
FTWARE: FASTSEQ for Windows Version 4.0
ID NO 113867
ENGTH: 236
                                                                                           AME/KEY: VARIANT
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ry Match
                                             -815-242-13867
                                                                           THER INFORMATION:
                                                                                                                                                                                              YPE: PRT
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; Sequence 8, Application US/09935943; Patent No. US20020120963A1; GENERAL INFORMATION: APPLICANT: Levin, Joshaa Z. APPLICANT: Hegrich, Lynette M. APPLICANT: Budziszewski, Gregory J. APPLICANT: Budziszewski, Gregory J. TITLE OF INVENTION: Herbicide Target Genes an FILE REFERENCE: PB/5-11509A; CURRENT APPLICATION NUMBER: US/09/935,943
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US-09-935-943-8
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US-09-792-251-8
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APPLICANT: Youngman, Philip
APPLICANT: Guzman, Luz-Maria
TITLE OF INVENTION: USE OF YACM AND YOEJ, ES
TITLE OF INVENTION: AND THEIR USE
FILE REFRENCE: 06286-140001
CURRENT APPLICATION NUMBER: US/09/792,251
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. US20020160364A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                     ERKGFLGTDDASLVEQMEGGSVRVVEGSYTNIKLTTPDDLTSAEAIMESES 227
                                                                                                                                                                                                                                                                                                          EGNPAV-TDEASALELL-GHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
                                                                                                                                                                                                                                                                                                                                                   ELIAEAEQTGAAILAVPVKDTIKRVQDLQVSETIERSSLWAVQTPQAFRLSLLWKAHAEA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24.8%; Score 297; DB 10; 36.8%; Pred. No. 2.5e-22;
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                                             and Methods
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Bes: Local :
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## AUTH: 232

## PRT

## ANISM: Rhodococcus erythropolis

## LANISM: LANISM: LANISM: LANISM: Rhodococcus erythropolis
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NGTH: 302
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OR APPLICATION NUMBER: PCT/EP01/08910
OR FILING DATE: 2001-08-01
OR APPLICATION NUMBER: US 60/222,779
OR FILING DATE: 2000-08-03
BER OF SEQ ID NOS: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           *AL INFORMATION:
SICANT: Bramucci, Michael G
E OF INVENTION: Genes Involved in Isoprenoid Compound Production
E REFERENCE: CL-1788
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 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 IFEEYEESIDVDLRFAIPGKERQDSVYSGLQEI-DVNSE--LVCIHDSARPLVNTEDVE-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 VVPAAGVGKRMQADRPKQYLPLAGKTVIEH---TLTRLLESDAFQKVAVAISVEDPY---
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                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       h 23.6%; Score 283.5; DB Similarity 34.2%; Pred. No. 9e-21; 80; Conservative 46; Mismatches
                                                                                                       QIDTLKNDPVGGILALSSHDTLKHVDG-DTITATIDRKHVWRALTPQMFKYGMLRDALQR 181
                                                                                                                                            ESVVADLGRASDVDVVGGGAERTDSVRAGLSA----AGDADFVLVHDAARALTPPALIAR 114
                                                                                                                                                                     -----SIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHL 122
                                                                                                                                                                                                                                                  AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPEL-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -WPELSIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHL 122
 -AGDVAATDDAALVERLGVSVQTIPGDALAFKITTPLDLVLAR
                                  TEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQ 224
                                                                       VVDALRAGSSAVIPVLPVTDTIKSVDVLGAVTGTPLRSELRAVQTPQGFSTDVLRSAYD-
                                                                                                                                                                                                                   ALVPAAGRGVRLGEKLPKAFVELGGCTMLARAVDGLRKSGAIDRVVVIVP-----PELV 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     --KVLKDGSAVGAAVLGVPAKATIKEVNSDSLVVKTLDRKTLWEMQTPQVIKPELLKKGF
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                      21.3%; Score 255.5; DB 1
35.0%; Pred. No. 4.8e-18;
tive 30; Mismatches 96
                                                                                                                                                                                                                                                                                                                           DB 12;
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; ORGANISM: Chlamydia pneumoniae US-10-289-762-621
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US-10-156-761-11503
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APPLICANT: HORIKAWA, HIROSHI
APPLICANT: SHIBA, TADAYOSHI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: SAKAKI, YOSHIYUKI
APPLICANT: HATTORI, WASHAHIRA
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-262
FILE REFERENCE: 249-262
CURRENT APPLICATION NUMBER: US/10/156,761
CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
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US-10-156-761-11503
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APPLICANT: OMURA, SATOSHI
APPLICANT: IKEDA, HARUO
TSHIKAWA, JUN
                                                                                                                                                                                                                                                  SEQ ID NO 621
LENGTH: 218
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 621, Application US/10:
Publication No. US20040006218A1
GENERAL INFORMATION:
APPLICANT: Griffais, R.
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PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 11503
LENGTH: 250
                                                                                       Matches
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                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve TITLE OF INVENTION: and treatment of infection FILE REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/10/289,762
CURRENT FILING DATE: 2003-03-27
                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 6849
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                                                                                    Local Similarity es 74; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120 IHLQIDTLKNDPVGGILALSSHDTLKHV------DGDTITATIDRKHVWRALTPQMFKY 172
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3 PTIQCWAVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDP 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAI-----SV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LDAH----ALPERTDFVVVPGGESRQESVKLGLDAL---PFGIDIVLVHDAARPLVPVDT 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GFDRDTLVRAHETVTDNVTDDASMVEQLGARVVVVPGHEBAFKVTRPLDLVLAE 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GMLRDALQRIEGNPA--VIDEASALELIGHKPKIVEGRPDNIKITRPEDLALAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VDAVIEAVRDGAPAVVPALPLADTVKQVEPAAVPGEPEPVVATPERARLRAVQTPQ----
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                                                                                    Conservative
                                                                            20.1%; Score 240.5; DB 12; Length 218; 32.9%; Pred. No. 1.5e-16; tive 41; Mismatches 92; Indels 19;
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US-09-738-626-6422
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                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: JP 99/377484
EXIOR PILING DATE: 1999-12-16
ERIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
EXIOR APPLICATION NUMBER: JP 00/280988
PLIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: OZAKI, AKIO
TETLE OF INVENTION: NOVEL POLYNUCLEOFIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
190
                                                                                    130 IARVVRKVHEGATAVÍPVLPVSDTIKRVSPDGGVVVDTPNRAELRAVQTPQGFLLSELVA 189
                                          178 ALOR -- TEGNEAV -- TDEASALELLGHKEKIVEGREDNIKITREEDLALAO 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 LAKEKOLTLVDDIRAABIIGKPSQLVFNKHPQIKISYPEDLTIAQ 215
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                                                                                                                                                                           LRKRGLLNDPEGVRVRLVHGGGERADSVWAGLQAISLDDATPDAIVLIHDSARALTPPGM 129
                                                                                                                                                                                                                                                                 ÄLLAAAGRGTRLGGPIPKAFVTLRERTLLERSLQAMLTSESVDBIIILVSPDMETYARDL
                                                                                                                                                                                                                                                                                                         AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE-DPYWPEL 67
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ANEKPFADPNPGFIPTDDASLMEWYGADVVCVQGDPMAFKVTTPIDMMLAQ 240
                                                                                                                              IHLQIDTLKNDPVGGILALSSHDTLKHV--DGDTITATIDRKHVWRALTPQMFKYGMLRD 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YOKOI, HARUHIKO
TATBISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -RTEGNEAUTDEASALELLGHKEKIVEGREDNIKITREEDLALAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --DLLETAEKIGATALASPIPYTIKORNP---VRTLDRDNLAIIHTPOCIKTEILREGLA
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OCHIAI, KEIKO
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                                                                                                                                                                                                                                                                                                                                                   18.6%; Score 223.5; DB 10; Length 256; ilarity 30.7%; Pred. No. 1.1e-14; Conservative 43; Mismatches 102; Indels 15;
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Search completed: January 29, 2004, 16:21:16
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Result
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match Length DB
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Gapop 10.0 , Gapext 0.5
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Copyright
GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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ALIGNMENTS

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RESULT 2 P83191 conserved hypothetical protein PA3633 [imported] - Pseudomonas aeruginosa (strain PA01) C;Species: Pseudomonas aeruginosa C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 17-Mar-2003 C;Accession: P83191 R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri	Qy 127 LKNDPVGGILALSSHDTLKHVDG-DTITATIDRKHVWRALTPQMFKYGMLRDALQR 181 :	Qy 9 AVVPAAGVGXRYQADRPXQYLPLAGKTVIEHTLITILESDAFQKVAVAISVEDPYWPELS 68 1	A;Map position: I C;Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol synthase C;Keywords: nucleotidyltransferase C;Keywords: nucleotidyltransferase Onery Match 47.9%; Score 574.5; DB 2; Length 232; Best Local Similarity 54.4%; Pred. No. 4.5e-41; Matches 124; Conservative 28; Mismatches 63; Indels 13; Gaps 5;	RESULT 1 C82311 C82311 C82311 C82311 C7-mosthyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60) - Vibrio cholerae C; Species: Vibrio cholerae C; Species: Vibrio cholerae C; Dato: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Mar-2003 C; Accession: C82311 C; Accession: C82311 R; Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vammathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000 A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae. A; Reference number: A82015; MUID: 20406833; PMID: 10952301

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 17-Mar-2003
C;Accession: G64156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein HI0672 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
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Mature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01,

A;Reference number: A32950; MUID:20437337; PMID:10984043

A;Accession: F83191

A;Status: preliminary
                                                                                                                                                                                                                     , D
                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:U32750; GB:L42023; NID:g1573668; PIDN:AAC22332.1; PIIA;Note: best homolog was a hypothetical protein from Rhodobacter capsulatus C;Superfamily: 4-diphosphocytidy1-2-methy1-D-erythritol synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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A;Molecule type: DNA
A;Residues: 1-225 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A;Reference number: A64000; MJID:95350630; PMID:7542800
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C;Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: G64156
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                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Matches 119;
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                      AIEDKQGAILAIPVTDTIKRADNQQCIVKTEDRSQLWQAMTPQFFPVDILRDALSTGIQQ 177
                                                                                                                                 L--DPKIQLVEGGTTRAESVLNGLNA---IAEKNAWVLVHDAARPCLQ----HADIDKLL
                                                                                                                                                             IAKHPDIITAPGGXERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPAVTDBASALBLIGHKPKIVEGRPDNIKITRPBDLALAQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKNDEVGGILALSSHDTLKHVDGD-TITATIDRKHVWRALTEQMFKYGMLRDAL-QRTEG
                                                                        --NDPVGGILALSSHDTLKHVDG-DTITATIDRKHVWRALTPQMFKYGMLRDALQR-TEG 184
                                                                                                                                                                                                                                                                                     AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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                                                                                                                                                                                                                                      AVLPAAGVGSRMQADKPKQYLTLLGKTLLEHTLDVMLSYPAVSKIILAVSKDDPYISTLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LAEDPVGGLLAVPARDTIKRSDRDGRVSETIDRSVVWLAYTPQMFRLGALHRALADALVA 189
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                                                                                                                                                                                                                                                                                                                                                                 44.2%; Score 530.5; DB 2; 52.5%; Pred. No. 2.2e-37;
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                                                                                                                                                                                                                                                                                                                                        28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypochetical protein ygbP [imported] - Escherichia coli (strain 0157H7, substrain C;Sp.coles: Escherichia coli (c;Sp.coles: Escherichia coli (c;Sp.cole: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-Mar-2003 C;Daccesion: B85924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: A91079
R;HE;Pishi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, gasewara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
BNA Res. 8, 11-22, 2001
BY The Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and B;Reference number: A99629; MUID:21156231; PMID:11258796
B;Accession: A91079
                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-236 <STO>
                                                                                                                                                                                                                                                                                                                                                              A;Title: Genome sequence of enterohemorrhagic Escherichia A;Reference number: A85480; MUID:21074935; PMID:11206551 A;Accession: B85924
                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Nature 409, 529-533, 2001
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C;Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol synthase
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A;Cross-references: GB:BA000007; PIDN:BAB37024.1; PID:g13363072; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
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A;Experimental source: strain O157:H7, substrain EDL933
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Best Local S
Macches 112
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Superfamily:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   178 GANITDEASAIELAGFRPHLVAGRSDNLKVTRPEDLALAEFYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 NPAVIDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYM 227
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                                                                           Similarity
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AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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50.2%;
                                                                              43.7%; Score 524.5; DB 2 50.2%; Pred. No. 7.6e-37;
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; Pred. No. 7.6e-37;
31; Mismatches 71
                                                     31; Mismatches
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J.D.; Rose, Potamousis,

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th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dow

(S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;

A;Title: Complete genome sequence of a multiple drug resistant

A;Reference number: ABO502; MUID:21534947; PMID:11677608

A;Accession: ABO856

A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Blattner, F.R.; Plunkett III,
.A.; Rose, D.J.; Mau, B.; Shao,
Science 277, 1453-1462, 1997
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                                                                                                                                     ;Accession: AE0856
;Parkhill, J.; Dougan, G.; James,
h, T.; Connerton, P.; Cronin, A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Keywords: nucleotidyltransferase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 Accession: G65055
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49.8%; Pred. No. 1.7e-36;
tive 31; Mismatches 72;
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Y.
                                                                                                                                          K.D.; T
                                                                                                                                          Thomson, N.R.;
, P.; Davies, R.
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                                                                                                                                          Pickard, I
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                                                                Skelton, J.; Stevens, Salmonella enterica su
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                                                                                                                                          D.; Wain, J, L.; White,
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М.;
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A;ACCULE PRELIM.
A;Statum: Prelim.
A;Molegule type: DNA
A;Molegule type: NA
- menidues: 1-241 < KUR>
- menidues: GB:AL590842;
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A; Residues: 1-236 < PAR>
A; Cross-references: GB:
C; Genetics:
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C;Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barr
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                                                                                                                                                                                                                                                                                                                                                     Superfamily: 4-diphosphocytidyl-2-methyl-D-erythritol
Keywords: nucleotidyltransferase
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Best Local
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Best Local (
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                                                                                                                                                                                                                                                                                                      Similarity
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                          NPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQ 230
                                                                                        NDFVGGILALSSHDTLKHVDG--DTITATIDRKHVWRALTPQMFKYGMLRDALQRT--EG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVVPAAGFGRRMQTECPKQYLSIGNKTILEHSVHALLAHPRVTRVVIAISPGDHRFAQLP
                                                                    CSQVGGILAAPVRDTMKRAEPGIQAIAHTVDRQDLWHALTPQLFPLELLKLCLSRALREG
                                                                                                                                         VAQDPRISTVYGGDQRANSVMAGIQ----LAGQAEWVLVHDAARPCLHLDDLSRLLSITE
                                                                                                                                                                                                                                              AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NDPVGGILALSSHDTLKHVD--GDTITATIDRKHVWRALTPOMFKYGMLRDALQR--TEG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                                                                                                                             AVLPAAGIGSRMLVDCPKQYLTVGGKTIIBHAIFSLLHHPRIQRVIVVIHPQDTQFSRLS
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#sequence_revision 02-Nov-2001 #text_change 17-Mar-2003
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                                                                                                                                                                                                                                                                                                  42.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                               PIDN:CAC92591.1; PID:g15981288;
                                                                                                                                                                                                                                                                                                    Score 512.5; DB Pred. No. 8e-36;
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Pred. No. 4.4
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C)Species: Buchnera sp. C, Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-Mar-2003 C, Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-Mar-2003 C, Accession: F84978 R, Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H. Nature 407, 81-86, 2000 Nature 407, 81-86, 2000 A, Title: Genome sequence of the endocellular bacterial symbiont of aphids B A, Reference number: A84930; MUID:20445173; PMID:10993077 A, Accession: F84978
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A;Fitle: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D81867
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein NMA1713 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 17-Mar-2003
C;Accession: D81867
R;Parkhill, J; Achtman, M; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajand, Nature 404, 502-506, 2000
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A;Experimental source: strain APS
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A; Residues: 1-237 < STO>
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;Superfamily: 4-di]
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  IHLQIDTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDAL 179
                                           TAFPQVRVWKN
                                                                                --WPELSIAKHPDIITAPGGKERADSVLSAL-KALE-DIASENDWVLVHDAARPCLTGSD 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIVPAAGIGSRMKIDVPKQYIKIQNRTILEHTLTTLLHPNIVQIIVSLNKKDNYFHKLS
                                                                                                                       ALIPAAGIGARFGADKFKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDTFADKVQ
                                                                                                                                                                AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPY-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISSNFRIISVVGGEKRINSVLSGLIVVKNV----DWVIVHDAVRPCLSYKDLEKLISIIK 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVVPAAGVGKRMQADREKQYLELAGKTVIBHTLTRLLESDAFQKVAVAISVEDPYWEBLS
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                                         GGOTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEA 119
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Pred. No. 1.:
                                                                                                                                                                                                                           Score 411.5; DB Pred. No. 2.5e-27
                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                            Length 229;
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Rajandream
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A;Cross-references: GB:AE002501; GB:AE002098; NID:g7226755; A;Experimental source: serogroup B, strain MC58 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Teutelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; Mitte, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qain, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A;Tille: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Experimental source: strain 9a5c
R;Singson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga,
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.B.A.; Carraro, D.M.; Carr
as-Neto, B.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                                                                                                    A,Ti:le: The genome sequence of the plant pathogen Xylella fastidiosa A,Reference number: A82515; MUID:20365717; PMID:10910347 A,Note: for a complete list of authors see reference number A59328 be
                                                                                                                                                                                                                                                                                                                                                                                         C;Accession: H82700
R;anchymous, The Xylella fastidiosa
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: NMB1513
C; Superfamily:
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A; Residues: 1-229 <TET>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change
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C;Species: Neisseria meningitidis
                                                                                                                                                                                                     A, Status: preliminary
A, Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 17-Mar-2003
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                                                                                                                                     A;Residues: 1-231 <SIM>
A;Cross-references: GB:AE003962; GB:AE003849; NID:g9106270; PIDN:AAF84102.1; GSPDB:GN001
                                                                                                                                                                                                                                                                           A;Accession: H82700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             conserved hypothetical protein XF1293 [imported] - Xylella fastidiosa (strain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64 --WPELSIAKHPDIITAPGGKERADSVLSAL-KALE-DIASENDWVLVHDAARPCLIGSD 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IHLQIDTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -AAENLDGITDEASAVEKLGVRPLLIQGDVRNLKLTQPQDAYIVRLLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIPAAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDTFADKVQ
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Pred. No. 3.7e-27;
9; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Consortium of the Organization for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis (strain MC58
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strain MC58.
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A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigu chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.E.; Marino, C.L.; Marques, M.V.; Martins, E.A.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak A;Authors: da Silva, A.D. de M.; de Rosa Jr., V.E.; de Sa, R.G.; W.A.; da Silvai, A.M.; Silva Jr., W.A.; da Silvai, R.F.; da Silva, A.M.; Silva Jr., W.A.; da Silveira, M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-228 <STO>
A;Cross-references: GB:AP001507; GB:BA000004; NID:g10172612; PIDN:BAB03826.1; GSPDB:GN00
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Mucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                             185
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                                                                                                                                                                                                                                                                                                                                                                                               10
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NPAV-TDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQ 230
                                                                                                                                                                                                                                                                        ----IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQI 124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPELSIAKHPDIITAPGGKBRADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQ 123
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                                                                                          ETAAKTH-AAVLAVPVKDTIKRVBGEAVLETMPREELWAVQTPQAFDLALIKQAHQKAEN 178
                                                                                                                                                    DTLKNDPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDALQRTEG 184
                                                                                                                                                                                                                                                                                                                                     VIPAAGQGKRMRAGHNKQFIELGGKPILAHTLAVFEQDDWCTNVVIVANEQEIEEMGELA
                                                                                                                                                                                                                                                                                                                                                                                            VVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESD-AFQKVAVAISVEDPYWPELS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EGNP-AVIDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQ 230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                29.5%; Score 353.5; DB 2; 37.0%; Pred. No. 1.9e-22; 44. Mismatches 86;
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18.58;
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Pred. No. 1.7e-24;
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A; Cross-references: EMBB:D26185; NID:g467326; PIDN:BAA05324.1; PID:g467478
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
R; Kunst, F:, Ogasawara, N:, Moszer, I:, Albertini, A.M.; Alloni, G:, Azevedo, V:, Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V:, Carter, N.M.; Choi
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A; Authors: Salberd, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,
Y.M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,
R; Rieger, M.; Rivolta, C.; Rocha, B.; Roche, B.; Rose, M.; Sado, T.; Scanton,
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,
A; Winters, P.; Wipat, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Zumstein, B.; Yoshikawa, H.; Danchin, A.
A; Terpstra, P.; Tognoh, A.; Tanaka, K.; Ashikawa, H.; Danchin, A.
A; Reference number: A69580; MUID:98044033; PMID:9384377
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #text_change 17-Mar-2003
C;Accession: D7044 #sequence_revision 08-May-1998 #text_change 17-Mar-2003
C;Accession: D7045;
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Grab
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental C; Genetics:
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A; Resjdues: 1-232 < KUN>
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A; Residues: 1-232 <OGA>
                                                                                                                                                      conserved hypothetical protein ad 1323 - Aquifex aeolicus
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ce: strain 168
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C;Genetics:
A;Gene: aq 1323
C;Superfamīly: 4-diphosphocytidyl-2-methyl-D-erythritol synthase
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-213 <AQF>
A;Cross-references: GB:AE000734; NID:g2983733; PIDN:AAC07307.1; PID:g2983746; GB:AE00065
A;Experimental source: strain VF5
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A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666; PMID:9537320
A;Accession: D70414
Search completed: January 29, 2004, 15:55:30 Job time: 6.79678 secs
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                                                                                                                                                         186 PAV-TOBASALBILGHKPKIVEGRPDNIKITRPEDLALAQFYM 227
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Result
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p57953 pasteurella
p57495 buchnera ap
p8d223 wiggleswort
Q8k9d6 buchnera ap
Q8p921 wanthomonas
Q8p918 wanthomonas
Q9p18 wanthomonas
Q9p18 ralstonia s
Q9p16 xylella fas
Q9p46 xylella fas
Q9p46 xylella fas
Q9p46 bacillus su
Q6755 bacillus su
Q6755 bacillus su
Q67143 aquifex aeo
Q8y149 anabaena sp
Q8uff4 a ispd/ispf
Q8y145 listeria mo
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Q871q2 vibrio
Q9kuj2 vibrio
Q9kuj2 pseudom
P57707 pseudom
   Q8y1x9
Q9uff4
Q8yab5
Q9x1b3
Q9x6b2
Q9zf40
P74323
Q8xhq3
P96864
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Q8fej5
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Q8z471
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2 fusobacteri
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GKTVIEH1 :: GKTILEH1	Score 605; DB Pred. No. 9.6e 1; Mismatches	095 ·	tute. as lor tremov ment (S ib.ch).	EMBL/GenBank/DDBJ databases. formation of 4-diphosphocyting CTP and 2C-methyl-D-erythrif). + 2-C-methyl-D-erythritol 4- the 5'-diphospho)-2-C-methyl-D- erpenoid biosynthesis pathwa HE ISDD FAMILY.	Kim J.J.	sequence update) annotation update) phosphate cytidylyltr hyl-D-erythritol synt)). Gammaproteobacteria;	, 237	AL I GNMENTS	MYCLE THEIN RHILO STRCO BRUME CHLPN CHLPN CHOAB CHLPN CHOAB CHOAB CHLPN CHOAB CHLPN CHOAB
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15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00108; -; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP005081; BAC60822.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Ta
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y.
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrionaceae; Vibrio.
NCBI_TaxID=670;
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15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cyridylyltransferase (EC (4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP cyridylyltransferase) (MCT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGEIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: Catalyzes the formation of 4-diphosphocytidy1-20-methy1-D-erythritol from CTP and 20-methy1-D-erythritol 4-phosphate (By similarity).

CATALYTIC ACTIVITY: CTP + 2-C-methy1-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methy1-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third ste SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collab
een the Swiss Institute of Bioinformatics and the EMBL outst
European Bioinformatics Institute. There are no restrictions
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234 AA;
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                                                           IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
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IALHPDVIRVAGGKERADSVLSGLNYV-SAQLPCEWVLVHDAARPCVTLNDIDRLIDVCC 128
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55.9%;
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30; Mismatches
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MEDLINE=20406833; PubMed=1092301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Gill S.R., Vanathevan J., Bass S., Qin H., Dragoi I., Seilers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
Ernser C.M.;
                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
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PROSTITE; PS01295; ISDD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
Complete proteome.
SEQUENCE 232 AA; 25901 MW; 44AA02420C724354 CRC64;
                                                                                                                                                                                                                   EMBL, AE004139; AAF93696.1; -. PIR; C82311; C82311. SSSP; Q46893; 1152. TIGR; VC0528; -.
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28-FBB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythrito1 4-phosphate cytidylyltransferase (BC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythrito1 synthase) (MEP cytidylyltransferase) (MCT).
                                                                                                                                                 PIRSF; PIRSF006765; DPCME_synth; 1.
                                                                                                                                                                 HAMAP; MF_00108; -; 1.
InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; IspD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=El Tor N16961 /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vibrionaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SPD OR VC0528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       L6-OCT-2001
                                                                                                                                                                                                                                                                                                       send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERVTHRITOL FROM CTP AND 2C-METHYL-D-ERVTHRITOL 4-PHOSPHALE (BY SIMILARITY).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5-diphospho)-2-C-methyl-D-erythritol PATHMAY: Monmevalonate texpenoid biosynthesis pathway; third standardty: BELONGS TO THE ISPD FAMILY.
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                                                                                                                                                                                                                                                                                                                    requires a license agreement (See http://www.isb-sib
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                                Score 574.5;
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Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saler M.H., Hancock R.E.W., Lory S., Olson M.V.;

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.";

Nature 406:959-964 (2000).

-I- FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRIFOL FROM CTP AND 2C-METHYL-D-ERYTHRIFOL 4-MOCONDAME (DV CIMITA DETEV).
                                                TIGREAMS; TIGRO0453; ispD; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                   HAMAP; MF 00108; ; 1.
InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; IspD; 1.
PIRSF; PIRSF006765; DPCME_synth; 1.
                                                                                                                                                                                                                                                                                         PIR; F83191; F83191.
HSSP; Q46893; 1152.
                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by arentities requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=ATCC 15692
MEDLINE=20437337;
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-p-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2-methyl-D-erythritol synthase) (MEP
                                                                                                                        TIGREAMS;
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16-OCT-2001 (Re
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CATALYTIC ACCIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third step.

SIMILARITY: BELONGS TO THE ISPD PAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European Bioinformatics Institute.
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MEDLINE=95350630; PubMed=7542800;

Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Fleischmann R.D., Adams M.D., White O., Clayton R.A., Merrick J.M., Karlavage A.R., Bult C.J., Tomb J.-P., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weiddann J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Weiddann J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fricchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnebm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O., Venter J.C.,
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                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib-entities requires a license agreement (See http://www.isb-sib-entities.
              HSSP; Q46893; 1152.
TIGR; HI0672; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C1-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
                                                        PIR:
                                                                      EMBL; U32750;
                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                               Science 269:496-512(1995).
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Fasteurellaceae; Haemophilus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Whole-genome random sequencing and assembly of Haemophilus influenzae
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                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol. PATHWAY: Normevalonate terpenoid biosynthesis pathway; third step. SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                         FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-PHOSPHATE (BY
                                                                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                        G64156; G64156.
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54.1%;
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Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli ol57:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001)

-!- FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-2C-methyl-Derythritol 4-phosphate.

-!- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

-!- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.
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PIRSF; PIRSF006765; DPCME_synth;
TIGRFAMs; TIGR00453; ispD; 1.
                                                                                                                                                                                                                                                                                                                                          STRAIN=0157:H7 / EDL933 / ATCC 700927;

KEDLINE=21074935; PubMed=1120655;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Posfai G., Hackett J., Klink S., Boutin A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Apodaca J., Blattner F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP cytidylyltransferase) (MCT) (CDP-ME synthetase).
                                                                                                                                                                                                                             STRAIN=0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=0157:H7 / R
                                                                                                                                                                                                                                                                                          Nature 409:529-533(2001).
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Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria;
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Best Local &
MEDLINE-22388234; PubMed-12471157;
Welch R.A., Burland V., Plunkett G. III, Redford P., Rowels Rasko D., Buckles B.L., Liou S.-R., Boutin A., Hackett Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N. Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
Mobley H.L.T., Donnenberg M.S., Blattner G., Mattheyenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                         Q8FEJS;
15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the Buropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-srsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TIGREAMS; TIGR00453; ispD; 1.

PROSITE; PS01295; ISPD; 1.

Transferase; Nucleotidyltransferase; Isoprene biosynthesis; Manganese; Cobalt; Complete proteome.

INIT_MET 0 0 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP; MF_00108; ; 1.
InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; ISpD; 1.
PIRSP; PIRSP006765; DPCM3_synth; 1.
TIGRPAMS; TIGR00453; ispD; 1.
                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=06:H1 / CFT073 / ATCC 700928;
                                                                                                                                                                                                                                                                                 Enterobacteriaceae,
NCBI_TaxID=217992;
                                                                                                                                                                                                                                                                                                                                        Escherichia coli 06.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                   cytidylyltransferase) (MCT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                             SPD OR C3314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A91079; A91079.
B85924; B85924.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NDPVGGILALSSHDTLKHVD--GDTITATIDRKHVWRALTPQMFKYGMLRDALQR--TEG
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BAB37024.1; -.
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No. 1e-38;
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(See http://www.isb-sib.ch/announce/
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                                                                                                         Hackett J.,
Perna N.T.,
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Best Local
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HANAF; MF 00108; -; 1.
HANAF; MF 00108; -; 1.
THERFAMS; TIGR00453; 1SpD; 1.
TIGRFAMS; TIGR00453; 1SpD; 1.
SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERI STRAIN-K12 / DH5-alpha; STRAIN-K12 / DH5-alpha; MEDLINE=99449755; PubMed=10518523; Rohdich F., Wungsintaweekul J., Fellermeier M., Sagn Kis K., Bisenreich W., Bacher A., Zenk M.H.; "Cytidine 5'-triphosphate-dependent biosynthesis of protein of Escherichia coll catalyzes the formation diphosphocytidyl-2-C-methylerythritol.";
                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythricol 4-phosphate cytidylyltransferase
(4-diphosphocytidyl-2-methyl-D-erythritol synthase) (MEI
cytidylyltransferase) (MCT) (CDP-ME synthetase).
                                                                                                                                                                                                                                                                                                                                                                                            ECOLI
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                                                                                                                                                                            Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                                                    Q46893;
01-NOV-1997
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INIT_MET 0 0 BY SIMI
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Transferase; Nucleotidyltransferase; Isoprene biosynthesis; Magnesium;
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                                                                                                                                                           NCBI_TaxID=562;
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                                                                                                                                                                                                                                  GPD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diphosphate + 4-{cytidine 5'-diphospho}-2-C-methyl-D-erythritol. COFACTOR: Magnesium, manganese or cobalt (By similarity). PATHWAY: Normevalonate terpenoid biosynthesis pathway; third step. SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            phosphate (By similarity).
CATALYTIC ACTIVITY: CTP +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 AA;
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                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25648 MW;
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Pred. No. 2.3e
32; Mismatches
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                                                                                                                            AND CHARACTERIZATION
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                                                                                                                                                                                               Enterobacteriales;
                                                                      Sagner S., Herz S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                      isoprenoids: YgbP of 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                               226
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PDB; 1152; 11-JUL-01.
PDB; 11NJ; 11-JUL-01.
PDB; 11NJ; 11-JUL-01.
ECGGene; EGG13110; 1spD.
ECGGene; EGG13110; 1spD.
INAMAP; MF 00108; -; 1.
INAMAP; MF 00108; -; 1.
INETERO 128; ISPD; synthase.
FEam; FF01128; ISPD; 1.
PIRSF; PIRSF006765; DPCME synth; 1.
TICHFAMB; TICHR0453; ispD; 1.
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Hilchard S.B., Bowman M.E., Kwiatkowski W., Kang I., Chow C.,

Hillo A.M., Cane D.E., Noel J.P.;

Kitructure of 4-diphosphocytidyl-2-C-methylerythritol synthetase

Involved in mevalonate-independent isoprenoid biosynthesis.";

Mat. Struct. Biol. 8:641-648(2001).

Mat. Struct. Biol. 8:641-648(2001).

Mat. Struct. Biol. 8:647-648(2001).

Mat. Struct. Biol. 8:647-648(2001).

MATHYLON: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-1-FUNCTION: CATALYZES THE FORMATION OF 2-TYTHRITOL 4-PHOSPHATE.

MATHYLON: CATALYZES THE FORMATION OF 2-TYTHRITOL 4-PHOSPHATE.

MATHYLON: CATALYZES THE FORMATION OF 2-TYTHRITOL 4-PHOSPHATE.

MATHYLON: CATALYZES THE FORMATION OF COBALT.

MANGANESE OR COBALT.

MANGANESE OR COBALT.

MATHYLON: Nonmevalonate terpenoid biosynthesis pathway; third step.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Cregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose I Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-K12 / W3110;
Kuzuyama T., Takagi M., Kaneda K., Dairi
"Formation of 4-(cytidine 5'-diphospho)-
2-C-methyl-D-crythritol 4-phosphate by 2
4-phosphate cytidylyltransferase, a new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                   Manganese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: OPTIMAL PH IS 8.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=K12
                                                                                                                                                               PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
Manganese; Cobalt; 3D-structure; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                  PIR; G65055; G65055
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: Homodimer.
                                                                                                                                                                                                                                                                                                                                                                                AF230736; AAF43207.1; -. AB037143; BAA90761.1; -. U29579; AAA69257.1; -. AB000358; AAC75789.1; -.
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   Kaneda K., Dairi T., Seto H.;
ne 5'-diphospho)-2-C-methyl-D-erythritol from
4-phosphate by 2-C-methyl-D-erythritol
wansferase, a new enzyme in the nonmevalonate
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K., Mayhew G.F
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP cytidylyltransferase) (MCT).
                                                                                                                                                                                                                                                                                             ISPD SALTI
Q8Z471;
 MBDLINE=21534947; PubMed=11677608; Parkhill J., Dougan G., James K.D., Thomson N. Churcher C., Mungall K.L., Bentley S.D., Holde Baker S., Basham D., Brooks K., Chillingworth
                                                                   STRAIN=CT18;
                                                                                 SEQUENCE FROM N.A.
                                                                                                                NCBI_TaxID=601;
                                                                                                                               Enterobacteriaceae;
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49.8%; Pred. No. 2.3e-38;
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ISPD SALTY QBZMF6; 28-FEB-2003 28-FEB-2003 28-FEB-2003

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HAMAD; MF 00108; -; 1.

InterPro. IPR001228; ISPD_Synthase.

Pfam; PF01128; ISPD; 1.

PIRSF; PIRSF006765; DPCME synth; 1.

TIGRPAMS; TIGR00453; ISPD; 1.

PROSITE; PS01295; ISPD; 1.

Transferase; Nucleotidyltransferase; Is
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MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
                                                                                                                                                                                                                                                                                                                             Complete
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriol. 185:2330-2337(2003)

PINCTION: Catalyzes the formation of 4-diphosphocytidyl-2C-methyl-D-crythritol from CTP and 2C-methyl-D-crythritol 4-phosphate (By similarity).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-crythritol 4-phosphate = CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-crythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-crythritol.

PATHWAY: Nonmevalomate terpenoid biosynthesis pathway; third stellar in SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cities requires a license agreement (Susend an email to license@isb-sib.ch).
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by non-profit institutions as long
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                                                                                 NDPVGGILALSSHDTLKHVD--GDTITATIDRKHVWRALTPQMFKYGMLRDALQR--TEG
                                                                                                                              LANHPQITVVDGGNERADSVLAGLQAV----AKAQWVLVHDAARPCLHQDDLARLLAISE
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                               NPAVTDEASALELIGHKPKI VEGRPDNIKI TRPEDLALAQFYM
                                                                                                                                                                                             AVVPAAGFGRRMQTECPKQYLSIGNKTILEHSVHALLAHPRVTRVVIAISPGDHRFAQLP
-ATITDEASALEYCGFHPALVEGRADNIKVTRPEDLALAEFYL
                                                                                                                                                AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
                                                                NSRVGG:
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                                                                ILAS PVRDTMKRGEPGKNA IAHTVERADI WHALTPQFFPREILHDCLTRALNEG
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                                                                                                                                                                                                                                                           43.0%; Score 515.5; DB 1;
49.8%; Pred. No. 6.4e-38;
70. Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                              Isoprene biosynthesis;
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                                                                                                                                                                                                                                                                                            DB 1;
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               ISPD_YERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HAMAP, MF_00108; -; 1.
InterPro; IFR001228; ISPD_synthase.
Pfam; PF01128; ISpD; 1.
PIRSF; PIRSF006765; DPCME_synth; 1.
TIGRPAMS; TIGR00453; ISpD; 1.
PROSITE; PS01295; ISPD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
Q8ZBP6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete proteome. SEQUENCE 236 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Salmonella enterica serovar Typhimurium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2-C-methyl-D-ezythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
cytidylyltransferase) (MCT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phosphate (By similarity).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third ste SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-2C-methyl-D-erythritol from CTP and 2C-methyl-D-erythritol 4-
                                                                                                                                          185
                                                                                                                                                                              126
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                                                                                                                                                                                                                                                                         IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128
                                                                                                                                    NPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYM
                                                                                                                                                                              NSRVGGILASPVRDTMKRGEPGKNAIAHTVERADLWHALTPOFFPRELLYDCLTRALNEG
                                                                                                                                                                                                                                                   LAMHPQITVVDGGNERADSVLAGLQAV----AKAQWVLVHDAARPCLHQDDLARLLAISE 125
                                                                                                                                                                                                                                                                                                                           AVVPAAGFGRRMQTECPKQYLSIGNKTILEHSVHALLAHPRVTRVVIAISPGDHRFAQLP 69
                                                                                                                                                                                                                                                                                                                                                     AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG?????; ispD.
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                                                                                                                                                                                                                 NDPVGGILALSSHDTLKHVD--GDTITATIDRKHVWRALTPOMFKYGMLRDALQR--TEG 184
                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 42.8%;
                                                                                                                                                                                                                                                                                                                                                                                                  32;
                                                                                                                                                                                                                                                                                                                                                                                                ; Score 513.5; |
; Pred. No. 9.6e
32; Mismatches
                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C4E631315492B80E
                 24 I
                                                                                                                                                                                                                                                                                                                                                                                                9.6e-38;
thes 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length 236;
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S., Layman D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3
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PIR; AC0408; AC0408.

HAMAP; MF 00108; -; 1.

InterPro; IPR001228; ISPD_synthase.

Pfam; PF01128; IspD; 1.

PIRSF; DFRS7006765; DPCME_synth; 1.

PROSITE; PS01295; ISPD; 1.

PROSITE; PS01295; ISPD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=CO-92 / Biovar Orientalis;

KEDLINE=21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Eaker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Leather S., Moule S., Cystom P.C.F., Quall M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.";

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deng W., Burland V., Plunkett G. III, Boutin A., Maylerna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C. Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G. Straley S.C., McDonough K.A., Nilles M.L., Matson J.S. Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phosphate (By similarity).
-!- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate =
-i- diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol
-!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third st
-!- SIMILARITY: BELONGS TO THE ISPD FAMILY.
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28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-crythritol 4-phosphate cytidylyltransferase (MEP
(4-dilphosphocytidyl-2C-methyl-D-crythritol synthase) (MEP
cytidylyltransferase) (MCT)
ISPD OR YP03361 OR Y0828.
                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=KIM5 / Biovar Mediaevalis;
NEDLINE=22137863; PubMed=12142430;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genome sequence of Yersinia pestis KIM.";

J. Bacteriol. 184:4601-4611(2002).

-i- FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-2c-methyl-D-erythritol from CTP and 2C-methyl-D-erythritol 4-
                                                                                                                                                  Complete proteome.
SEQUENCE 241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Versinia pestis
                                                                                                                                                                                  ransferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QUENCE
 13
                                     φ
                                                                                             Similarity
 AVLPAAGIGSRMLVDCPKQYLTVGGKTIIEHAIFSLLHHPRIQRVIVVIHPQDTQFSRLS
                                   AVVPAAGVGKRMQADRPKQYLFLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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                                                                                                                                                  26401 MW,
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                                                                                         42.78;
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                                                                       35;
                                                                                         Score 512.5;
Pred. No. 1.2
                                                                                                                                                  EF4CA6846BD4C261 CRC64;
                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       as long as its content is in no way removed. Usage by and for commercial ent (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions ng as its content is in
                                                                                                             DB 1;
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                                                                                                             Length
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IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128

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RESULT 12
ISPD PASMU
ID PASMU
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Best Local S
Matches 107
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                                                                                                                                                                                                                                                                                                                                                                                                             HAMAP; MF_00108; -; 1.
InterPro; IPR001228; ISPD_synthase.
Pfam; Pf01128; IspD; 1.
PIRSF; PIRSF006765; DPCME_synth; 1.
TIGRPAMs; TIGR00453; ispD; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
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2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.60)
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21145866; PubMed=11248100;
May 3.J., Zhang Q., Li L.L., Paust
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16-OCT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP; Q46893; 1152.
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mplete genomic sequence of Pasteurella multocida Pm70.";
DO. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-
METHYL-D-ERYTHRITOL FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-
PHOSPHATE (BY SIMILARITY).
CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate =
CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol.
DATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third stel
PATHWAY: Mommevalonate terpenoid biosynthesis pathway; third stel
SIMILARITY: BELONGS TO THE ISPD FAMILY.
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                                                                                                                                                                                                                                                                 Similarity
                                               IAKHPDIITAPGGKERADSVLSALKALEDIA--SENDWVLVHDAARPCLTGSDIHLQIDT 126
                                                                                                                                               AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELS
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LLTHPKIQLVEGGSSRADSVLNGLNAVKSAVQNSEDFWVMVHDAARPCLTHQDLDKLVQV 133
                                                                                                               AVVPAAGIGSRMOMDKPKOYLHIHGKTILEHTLSVLLGYPLIEKIILAVAANDPYISTCP
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i.4e-37;
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Best Local
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HAMAP; MF 00108; -; 1.
InterPro; IPR001228; ISPD_synthase.
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BUCAI
ISPD E
                                                                                                                                                                                                                                                                                                                                                Complete proteome. SEQUENCE 237 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P57495;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-DCT-2003 (Rel. 41, Last annotation update)
28-FEB-2003 (Rel. 41, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEF
                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMs; TIGRO0453; ispD; 1.
PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF01128; IspD; 1.
PIRSF; PIRSF006765; DPCME_synth; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 symbiotic bacterium)
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ISPD OR BU420.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AP001119; BAB13118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20445173; PubMed=10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishika
"Genome sequence of the endocellular bacterial symbiont
Buchnera sp. APS.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=Tokyo 1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae; Buchmera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: CATALYZES THE FORMATION OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL FROM CTP AND 2C-METHYL-D-ERYTHRITOL 4-PHOSPHATE (BY SIMILARITY).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third stesmillarity: BELONGS TO THE ISPD FAMILY.
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                                                                                                                                                                                                                                99;
                                                                                                                                                                                                                                                            Similarity
ISSNERIISVVGGEKRINSVLSGLIVVKNV----DWVIVHDAVRPCLSYKDLEKLISIIK
                                                 IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTIK 128
                                                                                                                AIVPAAGIGSRMKIDVPKQYIKIQNRTILEHTLTTLLHPNIVQIIVSLNKKDNYFHKLS
                                                                                                                                                     AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLITRLLESDAFQKVAVAISVEDPYWPELS
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                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                AA.
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                                                                                                                                                                                                                                                                                                                                                26922 MW;
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44.4%;
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                                                                                                                                                                                                                             50; Mismatches
                                                                                                                                                                                                                                                            Score 474.5;
Pred. No. 2.5
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les 67;
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                                                                                                                                                                                                                                                                                           237;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE 229 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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Nat. Genet. 32:402-407(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Wigglesworthia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
2-C-methyl-D-erythritol 4-phosphate cytidylyltransferase
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WIGBR
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Aksoy S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=36870;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION: Catalyzes the formation of 4-diphosphocytidyl-2C-methyl-D-erythritol from CTP and 2C-methyl-D-erythritol 4-phosphate (By similarity).

CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate = diphosphate + 4-(cytidine 5'-diphospha)-2-C-methyl-D-erythritol.

PATHMAY: Nonmevalonate cerpenoid biosynthesis pathway; third step.

SIMILARITY: BELONGS TO THE ISPD FAMILY.
130 DPVGGILALSSHDTLKHVDGDTITATIDRKHVWRALTPQMFKYGMLRDALQ-RTEGNPAV
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                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                VVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVEDPYWPELSI 69
                                                                                       LKNKKINIVIGGKSRTESVISALK----FVSKVDWVLVHDAVRPCLHKNDLNKLLKVINI
                                                                                                                                         AKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLKN 129
                                                                                                                                                                                                        ISVTDEASALEYCGYNPLLVLGSCRNIKITWPEDLVLANFYLK 231
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                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             26240 MM;
                                                                                                                                                                                                                                                                                                                   38.6%; Score 462.5; DB 1;
44.3%; Pred. No. 2.6e-33;
Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                           PROSITE; PS01295; ISPD; 1.
Transferase; Nucleotidyltransferase; Isoprene biosynthesis;
Complete proteome.
SEQUENCE 236 AA; 26967 MW; B3CCB1P88740DD25 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                   HAMAP; MF_00108; -; 1
InterPro; IPR001228;
Pfam; PF01128; IspD;
PIRSF; PIRSF006765; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the content is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S., Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.E.; "50 million years of genomic stasis in endosymbiotic bacteria."; Science 296:2376-2379(2002).

2: FUNCTION: Catalyzes the formation of 4-diphosphocytidy1-2C-aethy1-D-erythritol from CTP and 2C-methy1-D-erythritol 4-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE014116; AAM67955.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     phosphate (By similarity).
-!- CATALYTIC ACTIVITY: CTP + 2-C-methyl-D-erythritol 4-phosphate =
diphosphate +4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol
-!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; third st
-!- SIMILARITY: BELONGS TO THE ISPD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=22084549; PubMed=12089438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Buchnera aphidicola (subsp. Schizaphis graminum).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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15-SEP-2003 (Rel. 42, Last annotation update)
2-G-methyl-D-erythritol 4-phosphate cytidylyltransferase (EC 2.7.7.
(4-diphosphocytidyl-2C-methyl-D-erythritol synthase) (MEP
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Ms; TIGR00453; ispD; 1.
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 QR-TEGNPAVTDEASALELLGHKPKIVEGRPDNIKITRPEDLALAQFYMEQ 229
                                  NLIAITKNTKVGGILARPVCDTIKYSNRKNKTILHTIPRNQLWHALTPQLFPINLLRFCL
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                                                     LQIDTLKNDPVGGILALSSHDTLKHVD--GDTITATIDRKHVWRALTPQMFKYGMLRDAL 179
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Search completed: January 29, 2004, 15:50:40 Job time : 5.34994 secs

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Result
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q8dc60 vibrio vuln
Q8fej 5 escherichia
Q8ebr2 shewanella
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Q8d223 wiggleswort
Q9eyy4 klebsiella
Q64726 arabidopsis
Q46191 synechococc
Q48230 haemophilus
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Q481740 leptospira
Q8004 brucella su
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Q8fxz3	QBcjx6	Q9uzi7	Q8czf5	Q8z9s7	Q98cm6	Q9x364 bacillus		Q9cd44	Q8g5p1	Q8c934	Q9cef8	Q8i273 plasmodium		Q8br14	Q8s0p7	058136	0	Q8gpf2 streptococc	Q8nyi0	Q8ewc7	Q99wx2	Q8dpi2	Q97qe5	8ww660	Q8cq77	Q8g7e2	Q92cv0	Q8e4b4

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130 SHETGGILATPVRDTMKRANAQQMIDHTVDRNALMHALTPQMFKAEVLTDALSDALAQGV 189	129 NDPVGGILALSSHDTLKHVDG-DTITATIDRKHVWRALTDOMFKYGMLRDAL-QRTEGNP 186	70 IAQHPDIVRVAGGKERADSVLSALRFLSLQQQKADWVLVHDAARPCVAHQDIDALIERCS 129	69 IAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHLQIDTLK 128	ERLLSHPÁITQVVVÁVS	ADRPKOYLPLAGK	Query Match 50.5%; Score 605; DB 16; Length 237; Best Local Similarity 55.4%; Pred. No. 9.6e-44; Matches 124; Conservative 31; Mismatches 67; Indels 2; Gaps 2;		Complete proteome.	Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.	"Complete genome sequence of Vibrio vulnificus CMCP6.";	Knee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,	P6;	SEQUENCE FROM N.A.	(1) [1dx1D=0/2;	1111 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Hacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;			cytidyl-2-methyl-D-er:	(TrEMBLrel, 23, Last annotation	(TrEMBLiel. 23,	01-MAR-2003 (TrEMBLrel. 23, Created)		CBDC60 PRELIMINARY: PRT: 237 AA.	50 50

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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidyl-2C-methyl-D-erythritol synthase.
1SPD OR 503438.
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MEDLINE=2238234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., J.
Mayhew G.F., Rose D.J. Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donneuberg M.S., Blattner F.R.;

"Extensive mosaic structure revealed by the complete genome
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).

EMBL, AE015765; AAN81763.1;
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                               SEQUENCE FROM N.A.
STRAIN=MR-1;
                                                                                                    Alteromonadaceae; Shewanella.
NCBI_TaxID=70863;
                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                        Shewanella oneidensis.
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SEQUENCE 236 AA; 25779
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Enterobacteriaceae; Escherichia.
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     MEDLINE=22297686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LANHPRITYVDGGEERADSVLAGLKA----AGDAQWVLVHDAARPCLHQDDLARLLALSE 125
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                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
     PubMed=12368813;
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                                                                                                                                                           Gammaproteobacteria; Alteromonadales;
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Pred. No. 1.6e
32; Mismatches
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EMBL; AB065322; BAC24678.1; -. Complete proteome.
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Mat. Biotechnol. 20:1118-1123(2002).

EMBL, AB015780; AAN56435.1; -.
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Aksoy S.;
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Enterobacteriaceae; Wigglesworthia.
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Proternbacteriaceae; Klebsiella
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RESULT QBDL91 ID OR AC OR DT OI

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Best Local
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Makajima M., Enju A., Kamiya J
Hayashizaki Y., Shinozaki K.;
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**REDLINB=20300921; PubMed=10841550;

**REDLINB=20300921; PubMed=10841550;

**Rohdich F., Wungsintaweekul J., Eisenreich W., Richter G.,

**Rohdich F., Wungsintaweekul J., Eisenreich W., Richter G.,

**Schuhr C.A., Hecht S., Zenk M.H., Bacher A.;

**Schuhr C.A., Hecht S., Zenk M.H., Bacher A.;

**Biosynthesis of terpenoids. 4-diphosphocytidyl-2C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NATABIOOPSIS thaliana full-length cDNA.";
Submitted (NOV-2002) to the EMRI/Genmank/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Okada K., Kawaide H., Kuzuyama T., Takagi M., Seto H., Kam
"2-C-methyl-D-erythritol 4-phosphate cytidyltransferase.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                             SEQUENCE
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fam; PF01128; IspD; 1.
IGRFAMs; TIGR00453; ispD; 1.
250
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AC004136; AAC18936.2; -.
AF23D737; AAF61714.1; -.
AB037876; BAB21192.1; -.
AK118110; BAC42737.1; -.
Q46893; IINJ.
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ELVKSEG-LEVTDDVSIVEYLKHPVYVSQGSYTNIKVTTPDDLLLAERILSEDS
                                                                                                                                                         -WPELSIAKHPDIITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDIHL 122
                             -LORTEGNPAVTDEASALELIGHKPKIVEGRPDNIKITRPEDLALAQFYMEQQA 231
                                                                                                                                                                                          ILLAGGQGKRMKMSMPKQYIPLLGQPIALYSPFTFSRMPE-----VKEIVVVCDPFFRD 135
                                                              --KVLKDGSAVGAAVLGVPAKATIKEVNSDSLVVKTLDRKTLWEMQTPQVIKPELLKKGF
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Pred. No. 4e-16;
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ka M., Carninci P.,
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Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto Watanabe A., Iriquchi M., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsumo A., Nakazaki N., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi M., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi M., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.; Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shimpo S., Shi
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Pasteurellaceae; Haemophilus
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4-Diphosphocytidyl-2C-methyl-D-erythritol synthase.
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Cyanobacteria; Chroococcales; Synechococcus.
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Veiga-da-Cunha M., Merckx
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sphate reductase/CDP-ribitol
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           reductase-CDP-ribitol
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                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ATCC 9006;
Celis P., Moxon E., Eyssen H., v
"Genetic analysis of the Region
serotype a capsulation locus.";
Submitted (SEP-1994) to the EMBL
                                                                                                                                                                                                 MEDLINE=99194706; PubMed=10094675;
MEDLINE=99194706; PubMed=10094675;
Veiga-da-Cunha M., Merckx
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-0996 (TrEMBLrel. 23, Last annotation update)
01functional ribulose 5-phosphate reductase/CDP-ribitol
                                                                                                                                                                                       Pollens A., 'van Eldere J
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01-NOV-1996
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Pfam; PF01128; IspD; 1.
PROSITB; PS00061; ADH_SHORT; 1.
                        STRAIN=ATCC 9006;
                                                 SEQUENCE FROM N.A.
                                                                                                                  pyrophosphorlase
                                                                                                                                        encodes a bifunctional
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. STRAIN=ATCC 9006;
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                                                                                                                                                                                                                                                                                                                                                      Celis P.
                                                                                                                                                                                                                                                                                                                                                                            STRAIN-ATCC
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NCBI TaxID=727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Haemophilus influenzae.
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J. Bacteriol. 181:2001-2007(1999).
-:- SIMILARITY: BELONGS TO THE SHORT-CHAIN
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                                                                                              Bacteriol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 272; DB 2;
Pred. No. 7.3e-15;
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Haemophilus influenzae
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Best Local S
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01-MAR-2003 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Pfam; PF01128; ISpD; 1.
PROSITE; PS00061; ADH_SHORT; 1.
Oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Spirochaetes;
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InterPro; IPR001228; ISPD_synt)
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Nucleotidyltransferase; Trans
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                                                                                                                                                                                                                                                                                                                    Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                      Ren S.;
                                                                                                                                                                                                                                                                                                                                                STRAIN=56601 /
                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=173;
                                                                                                                                                                                                                                                                                                                                                                                                                      Leptospira interrogans.
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                         TEGNEAUTDEASALELLGHKEKIVEGREDNIKITREEDLALAQFY
                                                                                                          ESICASYLENEDRI-VQGGENRHSSMLCGLSVLD--FKDEDIILVHDAARPFVLADBLDS
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VDSIP-
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                                                                                                                                                                                                                                                                              238 AA;
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                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                               Serogroup
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62 MW; C02400F042434DFB CRC64;
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                                                                                                                                                                                                                      48;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                          Score 256; UD 1...
No. 6.5e-14;
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Pred. No. 1.1e-13;
                                                                                                                                                                                                                      Pred. No. 6.5e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGKERADSVLSALKALEDIASENDWVLVHDAARP-----
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                                                   SFLDREHVWFMKTPQGIRGDVLKELLTFS
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Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.
Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
Welson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.
Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
"The Brucella suis genome reveals fundamental similarities between
MEDLINE=21877339; PubMed=11882717;
Lazarevic V., Abellan F.X., Beggah S.,
"Comparison of ribitol and glycerol te
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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
2C-methyl-D-erythritol 2,4-cyclodiphosphate
synthase/4-diphosphocytidyl-2C-methyl-D-erythritoi synthase.
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Brucellaceae; Brucella,
NCBI_TaxID=29461;
                                                                                    SEQUENCE FI
STRAIN=W23;
                                                                                                                                                                                                Bacillus subtilis.
Bacteria; Firmicutes;
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Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
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Pred. No. 5.7e-13
18; Mismatches 9
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EMBL; AJ313428; CAC86109.1; -
InterPro; IPR001228; ISPD_synthase.
Pfam; P901128; ISPD; 1.
PROSITE; P801295; ISPD; 1.
Transferase; Nucleotidyltransferase.
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Q8FMI3, 01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          "The entire genomic sequence of Corynebacterium efficiens Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases. SMBL; AP005222; BAC19331.1; -
Hypothetical protein; Complete proteome. SEQUENCE 248 AA; 26727 MM; AC66FFF894BCEFF3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;

Kawarabayasi Y. Yamazaki J., Hino Y., Kikuchi H.,

Ikeo X., Suguki M., Mashima J., Itoh T., Yamagishi

Usuda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
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                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                           LTRRGLLNDPEGVRVRLVHGGGERADSVWAGLQAID----HDDAIVLIHDSAR-ALTPPGM
                                                                                                              ----SIAKHPD---IITAPGGKERADSVLSALKALEDIASENDWVLVHDAARPCLTGSDI 120
                                                                                                                                                                                                                            AVVPAAGVGKRMQADRPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVE-DPYWPEL
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                                                                                                                                                                      ALLAAAGRGTRIGGPIPKAFVTIRGRSIVERSIRAMITSEVVDEVIIIVSPDMEDYAREL
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28.7%;
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                                                                                                                                                                                                                                                                                  Score 248.5; DB
Pred. No. 3e-13;
7; Mismatches
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Pred. No. 2.8e-13;
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Baquero F., Berche P., Bloecker H., Brandt P., Chakrabortty T.,
A Baquero F., Berche P., Bloecker H., Brandt P., Chakrabortty T.,
A Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
A Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
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A Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
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A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
A Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
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"Comparative genomics of Listeria species.";
EL Science 294:849-852(2001).
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Best Local
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Hypothetical protein; Complete proteome.

SEQUENCE 236 AA; 26712 MW; ACD3CE124E9A5098 CRC64;
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InterPro; IPR001228; ISPD_synthase.
Pfam; PF01128; ISPD; 1.
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MEDLINE=21537279; PubMed=11679669;
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01-MAR-2002
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                                                                                                                                                                VQER 233
                                                                                                                                                                                                                                                                                                                                                  ----YGMLRDALQRTEGNPAVTDBASALELLGHKPKIVEGRPDNIKITRPEDLALAQFY 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YABILAGGKGTRMGNVNMPKQYLPLKGKPIIVHTIEKFILNDRFEKIIIATPKDWINHTQ 62
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(TrEMBLrel. 20, Last sequence up
(TrEMBLrel. 23, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 4.6e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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RESEQUENCE J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,

RA Eisen J.A., Nelson K.E., Paulsen I.T., Nelson W.C., Haft D.H.,

RA Hickey E.K., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,

RA HOlt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,

RA Nierman W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,

RA Vanmathevan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,

RA Vanmathevan J., Khouri H., Bryant D.A., Fraser C.M.;

"The complete genome sequence of Chlorobium tepidum TLS, a

Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).

RRT photosynthetic, anaerobic, green-sulfur bacterium.";

RR EMBL, AE012891; AAM72547.1; -.

DR TIGR; CT1317; -.

DR TIGR; CT1317; -.

DR FIGN; PF01128; ISPD, 11

PR PROSTTE; PS01295; ISPD, 1.

PR Complete proteome.

SQ SEQUENCE 246 AA; 27022 MW; D8DA46B55C2F5A56 CRC64;
                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlorobium tepidum.
Bacteria; Chlorobi; Chlorobia; Chlorobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8KCU3;
01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidyl-2C-methyl-D-erythritol synthase.
ISPD OR CT1317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CBI_TaxID=1097;
  99
99
                                           179
                                                                              126 D-DIARLSATHGACVPATKPKDTIKYVGCNPEIFGETLDRSRLLQVQTPQGFAPAKLIEA
                                                                                                                        121 HLQIDTLKNDPVGGILALSSHDTLKHV--DGDTITATIDRKHVWRALTPQMFKYGMLRDA 178
                                                                                                                                                                  66 IAKANGFTKITAIIEGGKERQDSIGNCMKLIEQEIENSGVMPDAILVHDGARPFIQEEEI
                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                        10 VVPAAGVGKRMQAD--RPKQYLPLAGKTVIEHTLTRLLESDAFQKVAVAISVED-PYWPE 66
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76; Conservative
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                                                                                                                                                                                                                                                   IIAASGVGKRMKLDGGRSKOMLEIGGOPVIWHTMKAFQEASTVESVYIATLPDSIPVFKE 65
-HRLAGEEQWYATDDAALVERYFPQQAIRIYETGYHNIKITTPEDVFIGE 233
                                LQRTEGNPA--VTDEASALELLGHKP--KIVEGRPDNIKITRPEDLALAQ 224
                                                                                                                                                                                                                                                                                                                             19.4%; Score 232:5; DB 16; Length 246; 33.0%; Pred. No. 6.9e-12; tive 39; Mismatches 98; Indels 17;
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                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                  125
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Search completed: January 29, 2004, 15:54:06 Job time : 19.2185 secs

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Published Applications AA:*

1: /cgn2=6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2-6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /cgn2-6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2-6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2-6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2-6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

7: /cgn2-6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

9: /cgn2-6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

10: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

11: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

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13: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

14: /cgn2-6/ptodata/1/pubpaa/US09E_PUBCOMB.pep:*

15: /cgn2-6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

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17: /cgn2-6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

16: /cgn2-6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

17: /cgn2-6/ptodata/1/pubpaa/US10E_PUB.pep:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  789580
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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533	556	572	572	580.5	582	582	584	584.5	616	620	638	1516	1516	1516	Score
35.2	36.7	37.7	37.7	38.3	38.4	38.4	38.5	38.6	40.6	40.9	42.1	100.0	100.0	100.0	Query Match 1
233	213	270	270	298	276	276	294	280	283	279	279	285	285	285	Query Match Length DB
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US-10-369-493-8419	US-10-369-493-19675	US-10-369-493-9359	US-10-369-493-9184	US-10-369-493-17751	US-10-369-493-16082	US-10-369-493-15690	US-10-369-493-15324	US-10-369-493-21079	US-10-369-493-802	US-10-369-493-201	US-10-369-493-13766	US-09-941-947A-12	US-09-934-868-74	US-09-934-903-8	ID
Sequence 8419, Ap	Sequence 19675, A	Sequence 9359, Ap	Sequence 9184, Ap	Sequence 17751, A	Sequence 16082, A	15690,	Sequence 15324, A	Sequence 21079, A		Sequence 201, App	~	Sequence 12, Appl	Sequence 74, Appl	Sequence 8, Appli	Description

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61 NPISGVPEQDDLTVRAANLIKSHTGCVRGVCIDIEKNIPMGGGLGGGSSDAATTLVVLNR 120

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-10-0	US-10-108-260A-3901	å	09-815-242-1	-09-882-227-	-10-264-213-2	-10-289-762-123	-10-369-493-	-09-738-62	-10-369-493-302	0-369-493-3	-10-369-493-6	-10-369-493-17	-09-712-363-1	9-493-260	-10-369-493-1515	-10-369-493-1467	-10-369-493-144	0-369-49	US-10-264-213-241	28-71	-10-156-76	-10-369-49	-10-369-49	-10-369-49	-369-493-9	0-369-4	US-10-369-493-7851	93-1	US-10-369-493-9956
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•	01,	2815, Ap	63,	œ	208, App	36,	'n	1515, Ap		16874, A	65, Appl	17829, A	186, App	2607, Ap	15150, A	14670, A	14419, A	11764, A	241, App	8, Appli	-	-	20265, A		•		7851, Ap	16541, A	56,

ALIGNMENTS

TABLE CHAMPELETY TO ANY OF A MANAGEMENT AND A STATE OF THE STATE OF TH		, ,
MDYAAGWGERWPAPAKLALALRITGRRPDGYHLLQTVFQMLDLCDWLTFHFVDDGRVTLR WDYAAGWGERWPAPAKLALALRITGRRPDGYHLLQTVFQMLDLCDWLTFHFVDDGRVTLR	- ц	₿ %
100.0%; Score 1516; DB 10; Length 285; larity 100.0%; Pred. No. 5.7e-156; Conservative 0; Mismatches 0; Indels 0;	Query Match Best Local Similarity Matches 285; Conser	
Amino acid sequences encoded by ORF4	; CTHER INFORMATION: Amino acid US-09-934-903-8	ŭ.,
16a	<pre>PEATURE:</pre>	٠. ٠.
	TYPE: PRT	~ ~
	SEC ID NO 8	• ••
Office 97	•••	** '
september 1, 2001 S: 24	PRIOR FILING DATE: September 1, NUMBER OF SEO ID NOS: 24	•• ••
IMBER: 60/229,907	PRIOR APPLICATION NUMBER: 60/229,907	••
: 2001-08-22	CURRENT FILING DATE: 2001-08-22	٠. ٠
FILE REFERENCE: CL1646 US NA CURRENT APPLICATION NUMBER: US/09/934.903	FILE REFERENCE: CL1646 US NA CURRENT APPLICATION NUMBER:	٠
Genes Involved in Isoprenoid Compounds Production	TITLE OF INVENTION: Genes Involved	••
piong	APPLICANT: Cheng, Qiong	
Rouviere, Pierre Picataggio, Stephen	APPLICANT: Rouvies APPLICANT: Picatac	
Tomb, Jean-Francois	•••	٠.
No. US20020102690Alton, Kelley C.	APPLICANT: No. US:	٠.
Schenzle, Andreas J.	••	٠,
Odom, J. Martin		٠.
Koffas, Mattheos	APPLICANT: Koffas,	٠.
	GENERAL INFORMATION:	٠. ٠
10n US/U99349U3 2690A1	Sequence 8, Application US/U99349U3 Patent No. US20020102690A1	
	US-09-934-903-8	g
	RESULT 1	꿩

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GENERAL INFORMATION:

APPLICANT: Koffas, Mattheos

APPLICANT: Codom, James M

APPLICANT: Codom, James M

APPLICANT: Codom, James M

APPLICANT: Coherale, Andreas J

TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN

FILE REFERENCE: CL1596 US NA

CURRENT APPLICATION NUMBER: US/09/934,868

CURRENT FILING DATE: 2001-08-22

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR APPLICATION NUMBER: 60/229,858

PRIOR APPLICATION NUMBER: 60/229,858

INUMBER OF ESG ID NOS: 81

SOFTWARE: Microsoft Office 97

SSO ID NO 74
                                                                                                                 RESULT 3
US-09-941-947A-12
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                                                        Sequence 12, Application US/09941947A Publication No. US20030003528A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 74, Application US/09934868 Patent No. US20020137190A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 285; Conserv
APPLICANT: Brzostowicz, Patricia C. APPLICANT: Cheng, Qiong APPLICANT: DiCosimo, Deana J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Methylomonas 16a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 285
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Pred. No. 5.7e-156;
Mismatches 0;
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Sequence 13766, Application US/10369493

Fublication No. US20030233675A1

GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PRO
ITILE OF INVENTION: EXPRESSION OF MICROBIAL PRO
ITILE OF INVENTION: DIANTS WITH IMPROVED PROPE

FILE REFERENCE: 38-10(52052)B

CURRENT APPLICATION NUMBER: US/10/369,493

CURRENT APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR APPLICATION NUMBER: US 60/360,039

PRIOR PILING DATE: 2002-02-21

NUMBER OF SEQ ID NOS: 47374

SEQ ID NO 13766

US-10-369-493-13766
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CURRENT FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
VUMBER OF SEQ ID NOS: 60
SOFTWARE: Microsoft Office 97
SEQ ID NO 12
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Best Loc
Matches
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Best Local
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                                   Query Match
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APPLICANT: Miller, Edward S. Jr.
APPLICANT: Odom, J. Martin
APPLICANT: Picataggio, Steve
APPLICANT: Rouviere, Pierre S.
APPLICANT: Rouviere, Pierre S.
TITLE OF INVENTION: CAROTEMOLD PRODUCTION FROM A SINGLE CARBON SOURCE
FILE REFERENCE: CL1903 US NA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Methylomonas 16a
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Local Similarity 49.
1es 135; Conservative
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Miller, Edward S.
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  42.1%; Score 638; DR
49.6%; Pred. No. 1.20
ative 41; Mismatches
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  DB 12;
1.2e-60;
hes 96;
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RESULT 6
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US-10-369-493-201
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Best Local Similarity
Matches 132; Conserv
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 201
LENGTH: 279
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Publication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
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                                                                                                                                                                                                                                                                                                                                                           65 NIIVRAARIIQDHAEKQSTGTQYRGADIHIHKRIPMGGGIGGGSSNAATVIIALNYHWQT 124
                                                                                                                                                                                                                                                                                                                                                                                                 71 DITVRAANLIKSH-----TGC-VRGVCIDIEKNIEMGGGIGGGSSDAATTIVVLNRIWGI 124
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                                                                                      FGEFESPASARKVÍNQAPEWMQGFVÁRGVNISPÍH 279
                                                                                                                               FAQFCNKEDAESALEGIKDRWIVFLAKGINQSALY 279
                                                                                                                                                                           PTDPELKRNSPIRTLPALLQAPFKNDCEPIARKRPREVEQLLSWLLEYTPSRLTGTGACV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.9%; Score 620; DB 12; ilarity 48.0%; Pred. No. i.le-58; Conservative 36; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 279;
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTBINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 802
LENGTH: 283
LENGTH: 283
TYPB: PRT
                                                                       ; CRGANISM: Xenorhabdus
US-10-369-493-21079
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US-10-369-493-802
                                                                                                                                     APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21079
LENGTH: 280
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Best Local Similarity
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                                                                                                                        TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 PVIFKDPELPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 GEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 WQCGLSMDELAEMGLTLGADVPVFVRGHAAFAEGVGBILTPVDPPEKWYLVAHPGVSIPT
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38.6%;
45.3%;
                                                                                                 nematophilus
                       Length 280;
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Query Match Best Local Similarity

Score 584.5; DB 12; Pred. No. 7.8e-55;

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US-10-369-493-15324
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LENGTH: 294
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Best Local
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILE REFERENCE: 38-10 ($2052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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ATRAAAEQAMAHLPGNLRAWVVEGAAHSPLLDALD 291
                                          CNKEDAESALEGIKDRWIVFLAKGINQSALYKKIE 283
                                                                                         <u>LTRDAAPAKIADFASGSLLDNAFÉPVLRRREPAIEAVFQALSRIGTPRLTGSGSGCFVEF</u>
                                                                                                                             LTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAI-DALLCYAEARLTGTGACVFAQF 248
                                                                                                                                                                            TLAELGLRIGADVPVFVRGHNAWAEGVGEKLTPISLFQAAYVLVDPGIHVPTPVLFQSQB 196
                                                                                                                                                                                                                                                                    DDLMYRAARALQIHAGTALGAELRVDKRIPAGGGFGGGSSDAATVLVALNALMGLGLPVD 136
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; Pred. No. 9.5e-55;
42; Mismatches 105;
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Query Match

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US-10-369-493-16082
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                                            US-10-369-493-16082
                                                                                                                        CURRENT APPLICATION UNDER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
IUMBER OF SEQ ID NOS: 47374
SEQ ID NO 16082
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SEQ ID NO 15690
LENGTH: 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 16082, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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Best Local Similarity
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
FITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
FITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                                                                                                                                       APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052) B
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                                                               ORGANISM: Xanthomonas
                                                                                           TYPE: PRT
                                                                                                            LENGTH: 276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               243 ATRAAAEQAMAHLPGNLRAWVVEGAAHSPLLDAL
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Length 276;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Xylella fastidiosa
US-10-369-493-17751
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 17751
LENGTH: 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17751, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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Local Similarity 46.3%;
                                                                                                 190
                                                                                                                                                                              130 ALMHTRLDVAVLAALGLRLGADVPVFVHGCNAWAEGVGECLTPMILPGAAYLLLDPGVCV 189
                                                                                                                                                                                                                      120
                                                                                                                                      180 NTGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSE-VVCKLYRPVKDAIDALLCYAEARLT 238
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                                                                                                                                                                                                                                                                                           60 RNPISGVPEQDDITVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLN 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11 WPAPAKINIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRV-TLRNPISGVPEQ 69
                                                       GTGACVFAQFCNKEDAESALEGIKDRWLVFLAKGLNQSALYKKLE 283
                     GSGSGCFVEFSTRDEAECALERLPYGLCAWVADGASRSPLLDVLK 294
                                                                                                                                                                                                                                                         GESVTGVVEADDLVVRAAYLLKYATNVHLGADIFVEKRIPVGGGFGGGSSDAATVLLVLN 129
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                                                                                                                                                                                                                                                                                                                                       VDDGVGW-SAWPAPAKLNIFLQITGRRVDGYHELQTVFRLLDWGDTIHLRVREDGQIHRI 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CNKEDAESALEGIKDRWIVFLAKGINQSALYKKI 282
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                                                                                               PTRELFLDPDLTRDASPATIGDFIAGTAFGNAFEPVLRRRESAVAGALDVLSEVGFARVT 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATRAAAEQAMAHLPGNLRAWVVEGAAHSPLLDAL
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1; Mismatches 105;
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; ORGANISM: Xylella fastidiosa
US-10-369-493-9359
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LENGTH: 270
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Best Local
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                                    TYPE: PRT
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; ORGANISM: Xylella fastidiosa
US-10-369-493-9184
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9359
LENGTH: 270
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                                                                                                                                                                                                             APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OP INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OP INVENTION: DIANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052)8
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
ERIOR FILING DATE: 2003-02-28
PRIOR PILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
                                                                                       CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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Similarity 47.4%;
28; Conservative 4
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Pred. No. 1.7e-53;
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RESULT 15
US-10-369-493-8419
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US-10-369-493-19675
; Sequence 19675, Application US/10369493
; Publication No. US20030233675A1
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID MOS: 47374
SEQ ID NO 19675
LENGTH: 213
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Best Local Similarity
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Best Local :
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatter, Steven C.
APPLICANT: Slatter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 ($2052)8
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ORGANISM: Nitrosomonas europaea
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                                                                                                                                               190 LTRNSAVVTMSDFLAGDNRNDCSBVVCKLYRPV 222
                                                                                                                                                                                         121 RIMALGLEIGADVPVFIYGRNAFAEGVGEELHAVDIPSAWYVVITPPVQISTAAVFTSKE 180
                                                                                                                                                                                                                  130 BLMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAEN 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 STRDEAECALERLPYGLCAWVADGASRSPL 270
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                                                                                                         LTRNTIPIKMAAFSMGQGHNDLEPVAMRM-QPV 212
                                                                                                                                                                                                                                                                          DLCVRAAKLLRQRFGRESLGVKIHLEKNIPLGGGLGGGSSDAATTLIALNRLWGINWKRE 120
                                                                                                                                                                                                                                                                                                                    DLTVRAANLLKSHTGCVR-GVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR 129
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  Application US/10369493
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36.7%; Score 556; DB 12; Length 213; 51.6%; Pred. No. 6.6e-52;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                  67;
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TYPE: PRT
; ORGANISM: Ralstonia metallidurans
US-10-369-493-8419
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
TILE REFERENCE: 38-10(52052)B
CURRENT EPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 8419
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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                                                                                                                                   228 ALLCYA-EARLTGTGACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSAL 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                              114;
                                                                                                                                                                                                                                                                          62 TILLALNRLWGVKLEREELWRIGLSLGADVPVFVFGQNAFABGVGEELTPVALPDSWFVV
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                                                                                           WIKNYSPHARMTGSGACVFARFEDEQTAQRVMERLPSEWDGRCVKSLSHHPL 233
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                                                                                                                                                                                 IHPRQHVPTAAIFSDERLTRNSPISIVADFAACTNKFAFGRNDLETIATAKFGEVARALE
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49.1%; Pred. No. 2.4e-49;
tive 35; Mismatches 77;
                       2004, 16:21:17
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Maximum Match 100%
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Maximum DB
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1516
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ALIGNMENTS

Result		Ouerv				
No.	Score	Match	Match Length DB	₽B	ID	Description
ь	1516	100.0	285	23	ABG61587	High growth metha
N	1516	100.0	285	23	AAE22304	Methylomonas 16a
Ļ	1516	200.0	285	23	AAU80328	Methylomonas 16a
4.	624	41.2	281	24	ABP78450	N. gonorrhoeae an
5	616	40.6	283	21	AAB11374	E. coli YCHB prot
δh	616	40.6	283	22	AAB68286	Amino acid sequer
7	332	21.9	283	23	ABP25586	Streptococcus pol
00	320	21.1	293	23	ABB50111	Listeria monocyto
y	302	19.9	299	23	ABP38503	Staphylococcus ep

WPI; 2002-452200/48

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96	96	96	96	98	98	101	105	110	110	110	111.5	114	114	114	115.5	125	127	140	176.5	178	195	195	204.5	216	216	223	224	263	267	9	268	270.5	275	277	278	
6.3	٠	٠					6.9			7.3	7.4	7.5	7.5	7.5	7.6		8.4	9.2	11.6	11.7	٧	N	13.5	4	•	•	14.8	•	•	•	•	17.8	٠	18.3	18.3	
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	treptococcus		Streptococcus pneu	Enterococcus faeca	Mevalonate pathway	wlar	.la typh:	thali	tha.	Arabidopsis thalia	od sn	Arabidopsis thalia	Ø		Fragment of homose	Haemophilus influe	.H. pylori GHPO 100		Amino acid sequenc	ÇD.		\mathbf{r}	ifidobacterium	Corynebacterium gl	C glutamicum prote	Propionibacterium	human	Amino acid sequenc		Arabidopsis thalia	ш			Amino acid sequenc	Rhodococcus erythr	

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RESULT 1
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                                                                                                                                                                                                                                                                                     01-SEP-2000; 2000US-229858P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            methane-containing environment;
nitrous oxide; terpenoid; anima;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ammonia; nitrate; nitrite; nitrogen; pigment; oxygen; landfill; methane-containing environment; waste water treatment system; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABG61587 standard; Protein; 285 AA.
                                                                                          Koffas M,
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                                                                                                                                                                                     g
                                                                                          Odom JM,
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                                                                                          Schenzle A;
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isoprenoid,

N-PSDB; ABK83266

04-SEP-2001;

2001WO-US27420

WO200218617-A2

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RESULT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a high growth methanotrophic bacterial strain, which grows on a Cl carbon substrate e.g. methane and methanol, and CC comprises a functional Embeden-Meyerhof carbon flux pathway comprising a gene coding a pyrophosphate dependent phosphofrutokinase enzyme or a 16s CC RNA. The bacterial strain is useful for the production of single cell CC protein and for the biotransformation of a nitrogen-containing compound, ce.g. ammonia, nitrate, citrite or nitrogen. It is also useful for the production of a feed product comprising a protein, carbohydrates and a CC pigment and for reducing oxygen demand, for removing nitrates and compound containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are present. The bacterial strain of the invention can be used as a conside with methane or methanol as a carbon source. It is also used in the production of biomass including proteins, carbohydrates and a wide converse of generating animal feeds), in production of terpenoid and caroteronid compounds, useful as pigments and as monomers in polymeric materials and in production of exopolysaccharides at high levels.

CC Sequences ABG61591-ABG61590 represent high growth methanotrophic conformal fervial strain of the invention.
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Best Local
                                                                                         Carotenoid; isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; anti-oxidant; steroid; flavour; fragrance; electro-optic application; aquaculture; enzyme; 4-diphosphocytidyl-2-C-methylerythritol kinase;
                                                                                                                                                                                                                                    Methylomonas 16a sp. 4-diphosphocytidyl-2-C-methylerythritol kinase
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functional gene encod
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gle cell proteins, grows on a Cl carbon substrate, and comprises a
ctional gene encoding in Embden-Meyerhof carbon pathway
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                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 285
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Methylomonas 16a

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Best Local Sim
Matches 285;
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The method comprises a transformed metabolising host cell, comprising suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. 4-diphosphocytidyl-2-C-methylerythritol kinase
                                 AAU80328 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes i the carotenoid biosynthetic pathway and which metabolize single carbon
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Odom JM, Picataggio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                GACVFAQFCNKEDAESALEGIKDRWLVFLAKGLNQSALYKKLEQG
                                                                                                                                                 GACVFAOFCNKEDAESALEGLKDRWLVFLAKGLNOSALYKKLEOG 285
                                                                                                                                                                                                TGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGT
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aggio SK,
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                                 Protein;
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100.0%; Pr
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Rouviere PE;
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Pred. No. 1.3e-155;
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Matches 285
                                                                                                                                                                                                                                                                                                                                                                              an isopremoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule encoding an isopremoid compound biosynthetic enzyme, and for the microbial production of isopremoid compounds. The molecules of the invention are also useful for regulating isopremoid biosynthesis in an organism and for producing recombinant organisms for producing various isopremoid compounds. The nucleic acid is also useful for feed additive, for the production of keratenoids and their derivatives, isopremoid intermediates, and as pure products useful as pigments, flavours and fragrances. The present amino acid sequence represents the Methylomonas 16a open reading frame 4 (ORF4) ychB/ispE (4-diphosphocytidyl-2-C-methylerythritol kinase enzyme) protein of the invention, as described
                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 71-72; 84pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid molecule encoding a isolated from Methylomonas 16a, useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive; keratenoid; pigment; flavour; fragrance; open reading frame 4; ORF4; ychB; 4-diphosphocytidyl-2-C-methylerythritol kinase enzyme; ispE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schenzle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          present invention relates to a new nucleic acid molecule encoding
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Best Local
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N-PSDB; AAC66044.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB11374 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agents, and related proteins, transformants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Labischinski H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
ACVFAQFCNKEDAESALEGLKDRWL-VFLAKGLNQSALYKKL 282
                                                                                                                                                                                                                                                                                                                                                                          DDLTVRAANEL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRL 121
                                                                                         PVIFKDPELPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
                                                                                                                                                                                                                                                                WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNT 181
                                                                                                                                              GEIFSAENLTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGIG
                                                                                                                                                                                                         WQCGLSMDELAEMGLTLGADVPVFVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
                                                                                                                                                                                                                                                                                                                        DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RWPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ehlert K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YHBC; YGBP; YGBB; YCHB; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 616; DB 21;
Pred. No. 5.3e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and antisense sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wieland
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                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 135; Conserv
                                                                                                                                                                                                                                                                                                                                          The present sequence represents an isopentenyl monophosphate kinase (IPK polymophide. The enzyme is an isoprenoid biosynthesis stimulator. The IPK polymucleotide is useful recombinant production of IPK, as a source of probes, primers and antisense sequences and for increasing/reducing expression levels of IPK in cells, particularly of essential oil plants, so as to increase flow through the isoprenoid biosynthesis pathway, resulting in increased production of e.g. pigments, vitamins and essential oils, also to increase resistance to pests and pathogens and to improve plant strength. Mutant forms of the IPK polymucleotide can be used to express forms of IPK that are resistant to IPK-targeted herbicides, and recombinant IPK can be used to screen for antibiotics, herbicides and antimalarial agents directed against IPK.
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                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                e.g. essential oils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New nucleic acid encoding isopentenyl monophosphate kinase, useful e.g. for making transgenic plants with increased synthesis of isoprenoids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Croteau RB,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 48-49; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isopentenyl monophosphate kinase; IPK; isoprenoid biosynthesis; pigment; vitamin; essential oil; pathogen resistance; antibiotic; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA368286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2001-308747/32
                   182
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                                                                                                                   64
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                                                                                                                                                                                                            10 RWPAPAKINIMIRITGRRPDGYHILQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ
                                                                                                                                                                                  d.
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GEIFSAENLTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLIGTG
                                                WQCGLSMDELAEMGLTLGADVEVEVRGHAAFAEGVGEILTEVDEPEKWYLVAHEGVSIET
                                                                                                                                                  DDLTVRAANLL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRL
                                                                         WGLGLSKRELMDLGLRLGADVÞVFVFGCSAWGBGVSEDLQAITLÞEQWFVIIKÞDCHVNT
                                                                                                                 DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
                                                                                                                                                                                QWPSPAKLNLFLYITGQRADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPVEGVEHE
                                                                                                                                                                                                                                                                                                                 283 AA;
                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                 40.6%; Score 616; DB 22;
47.9%; Pred. No. 5.3e-58;
tive 39; Mismatches 96
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                               Matches
                                                 Query Match
Best Local
                                                                                                                                        Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to determine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-OCT-2000; 2000GB-0026333.
24-NOV-2000; 2000GB-0028727.
07-MAR-2001; 2001GB-0005640.
                                                                                                                                                                                                                                                                                               The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory activity. (I), nucleic acids encoding (I), ABN65044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New Streptococcus protein for the treatment or prevention of or disease caused by Streptococcus bacteria, such as meningit for detecting a compound that binds to the protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB;
                                                                                                 Sequence
                                                                                                                               Streptococcus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 3188; 4525pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Telford J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001WO-GB04789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antiinflammatory; infection; vaccine; meningitis; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Streptococcus polypeptide SEQ ID NO 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GENO-)
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                                                 Similarity
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                                               Score 332; DB 23;
Pred. No. 3.4e-27;
                              Mismatches 107;
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Daniels J, Goebe
Dominguez-Bernal
                                                                                                                                                                                                                                                                                                                                     Buchrieser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Listeria monocytogenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABB50111 standard;
                                                                                                                                                                                                                                                                                                                                                                                         11-APR-2000; 2000FR-0004629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73 TV-RAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKREL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 terial; gene therapy; vaccine; biosynthesis; biodegradation; B12; bacterial infection; disease.
                                                                                                                                                                                                                                                  Voss
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Garcia Del Portillo F, Gomez-Lopez N;
Wehland J, Kaerst U, Entian K, Hauf
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Genomic sequence for Listeria monocytogenes, useful e.g. for and prevention of Listeria and related bacterial infections, related polypeptides for treatment

WPI; 2002-010914/01.

Claim 6; SEQ ID No 2816; 192pp; French.

The present invention relates to the genome sequence of Listeria minocytogenes RGD-e (see ABA03041). The genome sequence and fragments of it are useful for selecting probes and primers for detecting genes in L. monocytogenes and related organisms, and for studying genetic polymorphisms and other genomes. The present sequence is a protein encoded by the genome sequence of the present invention. Proteins expressed from the genome sequence are useful for raising specific antibodies, identification of L. monocytogenes and related organisms, are antibodies, identification of L. monocytogenes and related organisms, are for biosynthesis and biodegradation, especially biosynthesis of Vitamin E12. The genome sequence and proteins encoded by it are also useful for selecting compounds that regulate gene expression and cell replication and ۲ O

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABP38503;
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                                                                                                                                      Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:3348.
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                                                                                      Disclosure;
                                                                                                                                                                                                                                                                                                                 Doucette-Stamm LA,
                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-1997;
08-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Staphylococcus epidermidis; open reading frame; ORF; bacterial infection;
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                                                                                SEQ ID 3348; 267pp; English
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97US-064964P.
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Pred. No. 7.1e-26;
1; Mismatches 120;
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ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences

Claim 4; Page 72-73; 85pp; English

biosynthetic enzyme, altered activity -

and

for

producing

gene

products having enhanced

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N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the USPTO web site.
                                                                                                         New nucleic acid molecule from Rhodococcus erythropolis AN12 strain, useful for obtaining nucleic acid encoding isoprenoid compound
                                                                                                                                                                                              N-PSDB; AAD48798.
                                                                                                                                                                                                                                                                              Bramucci MG,
Rouviere PE,
                                                                                                                                                                                                                                                                                                                                                                                                                        24-APR-2001; 2001US-285910P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-APR-2002; 2002WO-US15033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhodococcus erythropolis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rhodococcus erythropolis ygbP (ispE) protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                biosynthesis;
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Tao L, Thomas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.9%;
                                                                                                                                                                                                                                                                                 Thomas SM;
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Pred. No. 6.5e-24;
51; Mismatches 103;
                                                                                                                                                                                                                                                                                                     Cheng
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                                                                                                                                                                                                                                                                                                           Kostichka
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                                                                                                                                                                                                                                                                                                        Nagarajan
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RESULT 11
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The present sequence represents an isopenteryl monophosphate kinase (II polypeptide. The enzyme is an isoprenoid biosynthesis stimulator. The IPK polynucleotide is useful recombinant production of IPK, as a source of probes, primers and antisense sequences and for increasing/reducing expression levels of IPK in cells, particularly of essential oil plants, so as to increase flow through the isoprenoid biosynthesis pathway, resulting in increased production of e.g. pigments, vitamins and essential oils, also to increase resistance to pests and pathogens
                                                                                                                                                                                                      New
                                                                                                                                                                                                                                                   WPI;
                                                                                                                                            Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      strain isoprenoid biosynthetic enzymes and polynucleotides encoding such proteins. Sequences of the invention are useful for regulating isoprenoid biosynthesis in an organism. They are useful for producti isoprenoid compounds and gene products having enhanced or altered activity. The present sequence is Rhodococcus erythropolis ygbp.
                                                                                                                                                                                                                                                                                                                                            04-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                        02-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isopentenyl monophosphate kinase; IPK; isoprenoid biosynthesis; pigment;
vitamin; essential oil; pathogen resistance; antibiotic; herbicide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of an isopentenyl monophosphatase kinase.
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                                                                                                                                                                                   nucleic acid encoding isopentenyl monophosphate kinase, useful emaking transgenic plants with increased synthesis of isoprenoids,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     present invention relates to novel Rhodococcus erythropolis AN12 in isoprenoid biosynthetic enzymes and polynucleotides encoding
                                                                                                                                                                       making transgenic plants essential oils -
                                                                                                                                                                                                                                                   2001-308747/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLR---NPISGVP-E
                                                                                                                                         Page 52-53; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                311 AA;
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Pred. No. 2.8e.
22; Mismatches
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No. 2.8e-21;
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essential oil; pathogen resistance; antibiotic; herbic;
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3; Mismatches
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Pred. No. 5.1e-21;
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The present sequence represents an isopentenyl monophosphate kinase (II polypeptide, The enzyme is an isopremoid biosynthesis stimulator. The IPX polynucleotide is useful recombinant production of IPX, as a source of probes, primers and antisense sequences and for increasing/reducing expression levels of IPX in cells, particularly of essential oil plants, so as to increase flow through the isopremoid biosynthesis pithway, resulting in increased production of e.g. pigments, vitamins and essential oils, also to increase resistance to pests and pathogens

source

New nucleic acid encoding isopentenyl monophosphate kinase, useful e.

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Example 8; Page 56-57; 62pp; English.

essential

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Matches 70
The present sequence represents an isopentenyl monophosphate kinase (IP) polypeptide. The enzyme is an isopentald biosynthesis stimulator. The IPX polymucleotide is useful recombinant production of IPX, as a source of probes, primers and antisense sequences and for increasing/reducing expression levels of IPX in cells, particularly of essential oil plants, so as to increase flow through the isopremoid biosynthesis pathway, resulting in increased production of e.g. pigments, vitamins and essential oils, also to increase resistance to pests and pathogens
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                                                                                                                                                                                                                                                                                                                            nucleic acid encoding isopentenyl monophosphate kinase, useful making transgenic plants with increased synthesis of isoprenoi. essential oils
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)B; AAF85084.
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                                                                                                                                                                                                                                                                     Page 60-61; 62pp;
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                                                                                                                                                                                                                                                                                                                                                            isoprenoids
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                                                                                                                                                                                                                                                                                                                                                                                       e.g.
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Best Local S
Matches 91
                                                                                                                                                                 21-SEP-1999;
11-OCT-1999;
05-NOV-1999;
                                                                                       Herz S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and to improve plant strength. Mutant forms of the IPK polynucleotide can be used to express forms of IPK that are resistant to IPK-targeted herbicides, and recombinant IPK can be used to screen for antibiotics, herbicides and antimalarial agents directed against IPK.
                                                                           Bacher A, Zenk M,
Herz S, Kis K, L
Wungsintaweekul J;
                                                                                                                                                                                                  04-AUG-1999;
21-SEP-1999;
                                                                                                                                                                                                                                    03-AUG-2000; 2000WO-EP07548
                                                                                                                                                                                                                                                         15-FEB-2001
                                                                                                                                                                                                                                                                                                                           genetic marker;
                                                                                                                                                                                                                                                                                                                                                          A. thaliana
                                                                                                                                                                                                                                                                                                                                                                                 04-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                     AAB70486;
                                                                                                                                                                                                                                                                                                                                                                                                                            AAB70486 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                         28-APR-2000;
                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                        Isoprenoid biosynthesis; 2C-methyl-D-erythritol-4-phosphate;
genetic marker; plant; isoprenoid biosynthesis inhibitor.
                                                                                                                       (ZENK/)
                                                                                                                                   (BACH/)
                                           2001-202774/20.
DB; AAF63675.
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                                                                                                                       ZENK
                                                                                                                                   BACHER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PAHQPVAQLRQVLQSAGGLGTMMSGSGPSVFTLCREQAEAEQVLAIAKEKLNDPDVDFWL 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TNEAYRAAQEMINNFPQAHDN-YGGVDITLTKHIPMAAGLAGGSADAAAVLVGEDLLWNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APAKLNUKLRITGRRPDGYHLLQTVFQMLDLCDWLTF--HPVDDGRVTL-RNPISGVPEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLSKREIMDLGLRLGADVPVFVFGCSAMGEGVSEDLQAITLPEQ---WFVIIK-PDCHVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLTRPELEQLAAQLGSDIPFCIGGGTAIATGRGEILD - - PLPDGNCFWVVLAKHRSIEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDLTVRAANIL-----KSHTGCVRGVCIDIBKNLPMGGGLGGGSSDAATTLVVLNRLWGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APAKINLFLEILGDRPDGFHELVMVLQSIALGDKITVRANGTDDIRLSCGDSPLAN--DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KLYRPVKDAIDALLCYA--EARLTGTGACVFAQFCNKEDAESALEGLKDR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TPWAYQTYRQKFGKNYLNDDQSQRARRKTTHAGPLLQGIQHRNPGQIASHIHNDLEKVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315 AA;
                                                                                                                                                                                                                                                                                                                                                         ychB
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                                                                                                                                                         2000DE-1020996
                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                                 99DE-1036663.
99DE-1045174.
99DE-1045175.
99DE-1048887.
99DE-1053309.
                                                                                                                                                                                                                                                                                                                                                          protein without
                                                                                     Luettgen
                                                                                                                                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                  Bisenreich
                                                                                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.8%; Score 270.5; 30.3%; Pred. No. 1.86 tive 49; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -GEIFSAENLTRNSAVVTM-----
                                                                                       Ä,
                                                                                                                                                                                                                                                                                                                                                                                                                            316
                                                                                     th W, Feller
Rohdich F,
                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                          leader sequence
                                                                                     Fellermeier M,
ich F, Sagner S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            109;
                                                                                     Fischer M, H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --SDFLAGDNRNDCSEVVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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                                                                                                   Hecht
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Enzymes which operate in the alternative isoprenoid pathway downstream from 2C-methyl-D-erythritol-4-phosphate, useful for screening a chemical library for inhibitors of the biosynthesis of isoprenoids -

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Best Local
04-AUG-1999;
21-SEP-1999;
21-SEP-1999;
11-OCT-1999;
05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2C-methyl-D-crythritol-2,4-cyclopyrophosphate or
4-diphosphocytidyl-2C-methyl-D-crythritol-2-phosphate, or their salts
are useful for screening for inhibitors of the biosynthesis of
isoprenoids. Herbicide resistant enzymes can be used as genetic markers
in any cell that is normally sensitive to the inhibitory effects of
herbicide formation. Methods from the present invention can be used to
produce herbicide resistant enzyme variants which can be incorporated
into plants to confer selective herbicide resistant on the plants. The
methods are also useful for controlling weed by cultivating crops
containing herbicide-resistant genes in the presence of weed-controlling
effective amounts of herbicides. The inhibitors are used for inhibiting
the biosynthesis of isoprenoids in plants, bacteria or protozoa. The
present sequence represents the Arabidopsis thaliana ychB protein without
leader sequence, which is given in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes functional enzymes (I) which operate in the alternative isoprenoid pathway downstream from 2C-methyl.D-erythritol-4-phosphate. (I) can be used as isoprenoid biosynthesis inhibitor. The enzymes are useful for screening a chemical library for inhibitors of the biosynthesis of isoprenoids.
                                                                                                           03-AUG-2000;
                                                                                                                                               15-FEB-2001
                                                                                                                                                                                WO200111055-A1
                                                                                                                                                                                                                    Arabidopsis thaliana
                                                                                                                                                                                                                                                     Isoprenoid biosynthesis; 2C-methyl-D-erythritol-4-phosphate; herbicide; genetic marker; plant; isoprenoid biosynthesis inhibitor.
                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana ychB protein
                                                                                                                                                                                                                                                                                                                                               04-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                   AAB70487;
                                                                                                                                                                                                                                                                                                                                                                                                                    AAB70487 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 12a; Annex Ea; 194pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -diphosphocytidyl-2C-methyl-D-erythritol,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     131 LMDLGLRIGADVPVFVFGCSAWGEGVSEDLQAITLP---EQWFVIIKPDCHVNTGEIFSA 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DITVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APAKUMLMIRITGRREDGYHLLQTVFQMLDLCDMLTEH-PVDDGRVTLRNPISGVP-EQD 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENLTRNSAVVIMSDFLAGDNRNDCSEVVC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLIIKALNLYRKKTGSNRFFWIHLDKKVPTGAGLGGGSSNAATALWAANELNGGLVTENE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPCKINVFLRITGKREDGFHDLASLFHVISLGGTIKFSLSPSKSKDRLSTNVQGVPVDGR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRIDQTSNINPLT-LLKNVTSNGVSQSIC 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   iQDWSSEIGSDIPFFFSHGAAYCTGRGEIVQDLPPPFFLDLPMVLIKPREACSTAEVYKR 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316
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                                                                                                             2000WO-EP07548
                                                                                                                                                                                                                                                                                                                                               (first entry
                     99DE-1036663.
99DE-1045174.
99DE-1045175.
99DE-1048887.
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                                                                                                                                                                                                                                                                                                                                                                                                                      383 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 268; DB 22;
Pred. No. 3.5e-20;
2; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 316;
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Search completed: January 29, Job time : 28.0514 secs

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CC 4-diphosphocytidy1-2C-methy1-D-erythrito1.

CC 4-diphosphocytidy1-2C-methy1-D-erythrito1-2-phosphate, or their salts

CC 4-diphosphocytidy1-2C-methy1-D-erythrito1-2-phosphate, or their salts

CC are useful for screening for inhibitors of the biosynthesis of

CC are useful for screening for inhibitors of the biosynthesis of

CC in any cell that is normally sensitive to the inhibitory effects of

CC in any cell that is normally sensitive to the inhibitory effects of

CC produce herbicide resistant enzyme variants which can be incorporated

CC into plants to confer selective herbicide resistant on the plants. The

CC containing herbicide-resistant genes in the presence of weed-controlling

C effective amounts of herbicides. The inhibitors are used for inhibiting

C the biosynthesis of isoprenoids in plants, bacteria or protozoa. The

C present sequence represents the Arabidopsis thaliana ychB protein,

C which is given in an example from the present invention.
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local (
                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the alternative isoprenoid pathway downstream from 2C-methyl-D-crythritol-4-phosphate. (I) can be used as isoprenoid biosynthesis inhibitor. The enzymes are useful for screening a chemical library for inhibitors of the biosynthesis of isoprenoids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enzymes which operate in the alternative isoprenoid pathway downstream from 2C-methyl-D-erythritol-4-phosphate, useful for screening a chemical library for inhibitors of the biosynthesis of isoprenoids -
                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacher A, Zenk M,
Herz S, Kis K, Lu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M-PSDB; AAF63680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-APR-2000; 2000DE-1020996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes functional enzymes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 12b; Annex Eb; 194pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mungsintaweekul J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACH/) BACHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZENK/) ZENK
                                   188
                                                                       197
                                                                                                          131
257
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                                                                                                                                                                                    71
                                                                                                                                                                                                                       77
                                                                                                                                                                                                                                                           13
                                                                                                                                                                                                                                                                                               l Similarity
69; Conserv
                                                                                                       LMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLP---EQWFVIIKPDCHVNTGEIFSA 187
                                 ENLTRNSAVVIMSDFLAGDNRNDCSEVVC 216
                                                                                                                                                DLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRE 130
                                                                                                                                                                                                                       SPCKINVFLRITGKREDGFHDLASLFHVISLGGTIKFSLSPSKSKDRLSTNVQGVPVDGR
                                                                                                                                                                                                                                                       APAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFH-PVDDGRVTLRNPISGVP-EQD
LRLDQTSNINPLT-LLKNVTSNGVSQSIC
                                                                       LQDWSSEIGSDIPFFFSHGAAYCTGRGEIVQDLPPPFFPLDLPMVLIKPREACSTAEVYKR 256
                                                                                                                                                                                                                                                                                                                                                                        383
                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Luettgen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eisenreich W,
                                                                                                                                                                                                                                                                                                                 17.78;
                                                                                                                                                                                                                                                                                                 42;
                                                                                                                                                                                                                                                                                                 Score 268; DB 22;
Pred. No. 4.6e-20;
2; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              h W, Fellermeier M, i
Rohdich F, Sagner S,
                                                                                                                                                                                                                                                                                                                                    Length 383;
                                                                                                                                                                                                                                                                                                     Indels
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, Schuhr CA;
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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
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270.5
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589.5
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/cgm2_6/ptodata/1/iaa/6B_COMB.pep:*
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US-09-434-774-12
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PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/09
PRIOR RILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 30806
LENGTH: 294
TYPE: PAT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30806
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                                                                                                                                             RNSAVVTMSDFLAGDNRNDCSEVVCKLYRFVKDAIDALLCYAEARLTGTGACVFAQFCNK 251
                                                               AEADKVSALLPDHLQRFVAKGSNISMLHRKLE
                                                                                                                                                                                                                                                    LIVRAARGIQEASGSPQGVDIWLDKRLPMGGGIGGGSSDAATTLLALNHLWQLGWDEDRI 139
                                                                                                                                                                                                                                                                                                                PAPAKLMLFIHILGRRDDGYHBLQTLFQFLDHGDELHFBARQDGQVRLHTBIAGVPHDSN 79
                                                                                                                            RDSPAIKVRTVLEGDSRNDCQPVVERRYPEVRNALILLNKFVSARLTGTGGCVFGSFPNK
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51.8%;
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Pred. No. 1.8e-65;
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Sequence 6, Application US/09434774A

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US-09-434-774-6
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CURRENT FILING DATE: 199-11-04
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 283
TYPE: DET.
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4670
LENGTH: 283
TYPE: PRT
ORGANISM: Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ISOPENTEN
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USB
FILE REFERENCE: wsur14448
                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 119; Conserv
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Best Local Similarity
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Patent No. 6562958
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                                                                             70 DDLTVRAANLLIKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTIVVLNRLWGLGLSKR 129
                                                                                                                                           RWPAPAKLNLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDITVRAANIL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTILVVLNRL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WQCGLSMDSLAEMGLTLGADVPVFVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
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                                         QNLIYRAAQILRPHAQNPCGLHIKIEKNIPMGAGLGGGSSNAATTLIVLNQLWQCGLTEE 127
                                                                                                                    RVPSPAKLNLFLHITGRRENGYHELQTIFQLIDLYDWMTFTPISEDEIQIEG-LGEVQLE
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ELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAEN 189
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                                                                                                                                                                                               Score 589.5; DB (
Pred. No. 8.2e-57,
8; Mismatches 8;
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Pred. No. 9.7e-60;
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                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                 89.
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RESULT 4
US-09-134-001C-3348
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                                                                                                                                                                                       Sequence 2, Application US/08596111B Patent No. 5824873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID NO 3348
LENGTH: 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Parent No. 6380370
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seguence 3348, Application US/09134001C Parent No. 6380370
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR PILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND
TITLE OF INVENTION: EPIDERMIDIS FOR
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/134,001C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE:
                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 25
              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                   APPLICANT: Lawrence, Susan D.
APPLICANT: Moore, Gloria A.
APPLICANT: Schuch, Wolfgang W.
TITLE OF INVENTION: DNA, CONSTRUCTS, TITLE OF INVENTION: DERIVED THEREFROM
                                                                                                                                                  APPLICANT:
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                            191
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                                                                                                                                                                                                                                                                                                                                                                                       TEEHIVHNEKCKQALENNDYHLLCNSLSNRLEPVSMAMHPDIKKIKDNMLQCGADGALMS
                                                                                                                                                                                                                                                                                                                                                                                                                          TRNSAV------VTMSDF--LAGDNRNDCSEVVCKLYRPVKDAIDALL-CYAE-ARLT 238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APAKLMIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVP-EQDD 71
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White & Durkee
                                                                                                                                                      Donald
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                                                                            CELLS AND
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COUNTRY: USA

STREET:

P.O. Box 4433

Houston

Texas

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; TYPE: PRT
; ORGANISM: Lycopersicon esculentum
US-09-434-774-10
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US-08-596-111B-2
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/09434774A Patent No. 6235514
                                                                                        SEQ ID NO 10
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FILING DATE: 10-APR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9315751.9
FILING DATE: 30-JUL-1993
AITORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UFLA:068
TELECOMMUNICATION INFORMATION:
                                                                                                                                                     FILE REFERENCE: wsur14448
CURRENT APPLICATION NUMBER: US/09/434,774A
CURRENT FILING DATE: 1999-11-04
                                                                                                                                                                                                             APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID WOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USE
                                                                                                           NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (512)418-3000
TELEFAX: (512)474-7577
INFORMATION FOR SEQ ID NO: 2:
                                                                 LENGTH: 401
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LENGTH: 401 amino acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 77210-4433
COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
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TOPOLOGY: line-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 18.3%; Score 277; DB 2; Local Similarity 34.0%; Pred. No. 4.5e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 LMDLGLRLGADVFVFVFGCSAWGEGVSEDLQAITLFEQW---FVIIKPDCHVNTGEIFSA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              153 NLIIKALNLYRKKTGTDNYFWIHLDKKVPTGAGLGGGSSNAATTLWAANQFSGCVATEKE
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                                                                                                             PatentIn Ver.
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CURRENT APPLICATION NUMBER: US/09/434,774A
CURRENT FILING DATE: 1999-11-04
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 383
TYPE: PRT
ODCANTON
                                                                                                                                                                                                     RESULT 8
US-09-434-774-16
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                                                                                                                               Sequence 16, Application US/09434774A Patent No. 6235514 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USE
FILS REFRENCE: WSUL1448
CURRENT APPLICATION NUMBER: US/09/434,774A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 18.3%; Similarity 34.0%; 71; Conservative 4:
                                                                                                                                                                                                                                                                                                                                          ENLTRNSAVVIMSDFLAGDNRNDCSEVVC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                   LMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLP---EQWFVIIKPDCHVNTGEIFSA 187
                                                                                                                                                                                                                                                                                                                                                                                     LODWSSEIGSDIPPPPSHGAAYCTGRGEIVODLPPPPPLDLPMVLIKPREACSTAEVYKR 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPCKINVFLRITGKREDGFHDLASLFHVISLGDTIKFSLSPSKSKDRLSINVQGVPVDGR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQLDLSSKVDPLS-LLEKISTSGISQDVC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENLTRNSAYVIMSDFLAGDNRNDCSEVVC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLTVRAANILKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRE 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPCKINVFLRITSKRDDGYHDLASLFHVISLGDKIKFSLSPSKSKDRLSTNVAGVPLDER 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LQEWSGEIGSDIPFFFSHGAAYCTGRGEVVQDIPSPIPFDIPMVLIKPQQACSTAEVYKR 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.1%; Score 275; DB 3 33.5%; Pred. No. 7e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 277; DB 3; Length 401;
Pred. No. 4.5e-22;
3; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 3; Length 383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91;
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CURRENT FILING DATE: 1999-11-04

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US-09-434-774-2
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US-09-434-774-16
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Matches
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SOFTWARE: PatentIn Ver.
SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/09434774A Patent No. 6235514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: wsur14448
CURRENT APPLICATION NUMBER: US/09/434,774A
CURRENT FILING DATE: 1999-11-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Croteau, Rodney B
APPLICANT: Lange, Bernd M
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING ISOPENTENYL
TITLE OF INVENTION: MONOPHOSPHATE KINASE, AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver.
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Mentha piperita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 405
                                                                                                                                                                                                                                                                                                                                 Local Similarity
mes 76; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 91; Conserv
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                                                                                                                    130 EUMDIGIRIGADVPVFVFGCSAWGEGVSEDIQAITLP---EQWFVIIKPDCHVNTGEIFS 186
                                                                                                                                                              161 KNLIIKALNLERKKTGTDKHFWIHLDKKVPTGAGLGGGSSNAATALWAANQFSGCIATEK 220
                                                                                                                                                                                                                                               102 SPCKINVFLRITGKREDGFHDLASLFHVISLGDKIKFSLSPSKFNGSFVTN-VPGVPLDB 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        243 PAHQPVAQLRQVLQSAGGLGTMMSGSGPSVFTLCREQABAEQVLAIAKEKLNDPDVDFWL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              125 GLSKRELMDLGLRLGADVEVFVFGCSAWGEGVSEDLQAITLFEQ---WFVIIK-PDCHVN 180
                                                                                                                                                                                                                                                                     13 APAKLALMIRITGRR2DGYHLLQTVFQMLDLCDWLTF--HPVDDGRVTLRNPISGVP-EQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 TYLAYRAAQLMINNFPQAHDN-YGGYDITLTKHIPMAAGLAGGSADAAAVLVGLDLLWNL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 DDLTVRAANLL----KSHTGCVRGVCIDEEKNLPMGGGLGGGSSDAATTLVVLNRLWGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       315
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REREDQTSDEDPEVELEKISKGGISQDVCVNDLEPPAFEVVPSEKR-EKQRIAAAGRSQY 339
                                                                               DIQEWSGEIGSDIPFFFSHGAAYCTGRGEVVEDIPPPVPRDLSMVLMKPQEACPTGEVYK 280
                                                                                                                                                                                                     DDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLYRPVKDAIDALLCYA--EARLTGTGACVFAQFCNKEDAESALEGLKDR-----WL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-----SDFLAGDNRNDCSEVVC 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLTRPELEQLAAQLGSDIPFCIGGGTAIATGRGEILD--PLPDGNCFWVVLAKHRSIEVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APAKINLFLEILGDRPDGFHELVMVLQSIALGDKITVRANGTDDIRLSCGDSPLAN--DA 65
                                     AENLTRNSAVVTM------SDFLAGDNRNDCSEVVCKLYRFVKDAIDAL--LCY 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPWAYQTYRQKFGKNYLNDDQSQRARRKTIHAGPLLQGIQHRNPGQIASHIHNDLBKVVL
                                                                                                                                                                                                                                                                                                                            17.3%; Score 263; DB ilarity 30.2%; Pred. No. 1.6e Conservative 50; Mismatches
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                                                                                                                                                                                                                                                                                                                                                DB 3;
L.6e-20;
                                                                                                                                                                                                                                                                                                                                 104;
                                                                                                                                                                                                                                                                                                                                                                    Length 405;
                                                                                                                                                                                                                                                                                                                                 Indels
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; LENGTH: 99
; TYPB: PRT
; ORGANISM: Lactobacillus rhamnosus
US-09-634-238-305
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US-09-198-452A-1236
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TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

CURRENT FILING DATE: 1998-11-24

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
            Query Match
Best Local Similarity
                                                                                                                                                        SEQ ID NO 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 305, Application US/09634238 Patent No. 6544772
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                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/634,238
CURRENT FILING DATE: 2000-08-08
NUMBER OF SEQ ID NOS: 422
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Polynuclectides, materials incorporating TITLE OF INVENTION: them and methods for using them.
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
                                                                                                                                                                                                                                                             FILE REFERENCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123 LWARBIGSDVPFF 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 APAKLNIMIRITGRRPDGYHLIQTVFQMIDICDWLTFHPVDDGRVTLRNPISGVPBQDDL 72
36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   h 11.7%; Score 178; DB 4; Similarity 32.3%; Pred. No. 8.4e-12;
                                                                                                                                                                                                                                                                                                              Holland, Ross
O'Toole, Paul W.
Reid, Julian R.
Coolbear, Timothy
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                                                                                                                                                                             FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                           Havukkala, Ilkka J.
Bloksberg, Leonard,
Lubbers, Mark W.
                                                                                                                                                                                                                                                                                                                                                                                                                          Lubbers, Mark
Dekker, James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glenn, Matthew
Conservative
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10.6%; Score 160; DB 4;
44.4%; Pred. No. 4.9e-10;
ative 15; Mismatches 30
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                                      Length 99
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Patent No. 5753479
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 783 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/843,521
FILING DATE: 18-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38,891
REFERENCE/DOCKET NUMBER: P31457-6
TELSCOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 18-APR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRLEFAX: 610-270-5090
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                                                                                                                                                                                                                                                                                            h 6.0%; Score 91.5; DB 1; Length 783;
Similarity 22.4%; Pred. No. 0.38;
43; Conservative 34; Mismatches 76; Indels 3
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                                                                                                                                                  DVEVSSTLADVNRVLGTELSYADVXDVFRRLG----FGLSG----NADSFTVSVPR
                                                                                                                                                                                   SSDAATTIVVLNRLWGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLP- 166
                                                                                                                                                                                                                          GRLNLRSESSSRFEKGINVATVNEALDAÄASMIAELAGAT-----VRKGIVSAGELDTS
                                                                                                                                                                                                                                                         GRYTLRNPIS-----GVPEQDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGG
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     EGAGLTEIITYA 519
                                       ---AIDALLCYA 233
                                                                                                             EQWFVIIKPDCHVNTGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKD--
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                                                                          REWDITIEADLEEEIARIYGYDRLPTS---LPKDDGTAGE-----LTVIQKLRRQVRTIA 507
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             RESULT 14
US-09-134-001C-4141
; Sequence 4141, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
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APPLICANT: Lynn Doucette-Stamm et al
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TOPOLOGY: linear; NOLECULE TYPE: protein US-09-012-871-2
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US-09-012-871-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
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TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Seecham Corporation
STREET: 709 Swedeland Road
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Gimmi, Edward R
REGISTRATION NUMBER: 38.
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
STRANDEDNESS: sir
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CITY: King of Prussia
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508 EGAGLTBIITYA 519
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                                                                                                                                                408 DVEVSSTLADVNRVLGTELSYADVXDVFRRLG
                                                                                                                                                                                   108 SSDAATTLVVLNRLWGLGLSKRELWDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLP- 166
                                                                                                                                                                                                                      354 GRLALRSESSSRFEKGINVATVNBALDAAASMIAELAGAT-----VRKGIVSAGELDTS 407
                                                                                                                                                                                                                                                         55 GRVTLRNPIS-----GVPEQDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGG 107
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                                                                        RRWDITIEADLFEEIARIYGYDRLPTS---LPKDDGTAGE----LTVIQKLRRQVRTIA 507
                                                                                                         EQWFVIIKPDCHVNTGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKD-- 224
                                     ---AIDALLCYA
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US-09-252-991A-24594
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; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24594
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MATC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR PRICE PRIOR DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24594
LENGTH: 312
TYPER. DET
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT APPLICATION NUMBER: US 60/064,964
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
SEQ ID NO 4141
LENGTH: 315
TYPE: PRI
TYPE: PRI
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Patent No. 6551795
GENERAL INFORMATION:
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Best Local Similarity
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les 30; Conser
263
                                                                                                                                                 109 SDAATTIVVINRIMGIGISKREIMDIGIRIGADVEVEVEGCSAMGEGVSEDIQAITIPEO 168
                                                                                                                                                                                                           155 HPGCEGA-----PLSGGIPPRILLFVTAIVLHNIPEGMAVGVSAGAGLDEAMGLALGIAL 209
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                                                                                                                                                                                                                                                           50 HPVDDGRVTLRNPIS-GVPEQDDLTVRAANLLKSHTGCVRGVCIDIBKNLPMGGGLGGGS 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 ISGVPEQDD---LTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNR 120
                                                                                                    QDVPEGIVVALVLAGVGMSRFKAMLVGAASGIVEPLFAVLC-AWLVGLS---
WGLAAAAGAMLFVVTHEIIPESH 285
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                                               W-----FVI---IKPDCH 178
                                                                                                                                                                                                                                                                                                          5.7%; Score 86; DB 4; Length 312; nilarity 30.8%; Pred. No. 0.39; Conservative 15; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5.9%; Score 89; DB 4; Length 315; llarity 20.0%; Pred: NO. 0.19; Conservative 38; Mismatches 66; Indels
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Search completed: January 29, 2004, 15:57:05

Job time : 9.94468 secs

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Result
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Match
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Maximum Match 100%
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// Cgn2 6/ptcdata/1/pubpaa/USO7_NEW_PUB.pep:*
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// Cgn2 6/ptcdata/1/pubpaa/USO6_PUBCOMB.pep:*
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// Cgn2 6/ptcdata/1/pubpaa/USO9_PUBCOMB.pep:*
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2568,	w	e 2815,	10963,	Sequence 358, App	208, 3	36,	equence 10645,	e 4515	e 3024,	1687	æ	e 17829,	e 186, A	Ø	Ø	e 14670,	e 14419,	e 1:1764,	e 241,	e 8, Aj	e 11123,	Sequence 12283, A	quence 20265,	e 17097,	O	Φ	quence 7851,	e 16	Sequence 9956, Ap

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                                                                                                         Query Match
Best Local S
Matches 285
                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 24
SOFTWARE: Microsoft Office 97
SEQ ID NO 8
LENGTH: 285
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CURRENT APPLICATION NUMBER: US/09/934,903
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: September 1, 2001
PRIOR FILING DATE: September 1, 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPIICANT: Koffas, Mattheos
APPIICANT: Odom, J. Martin
APPIICANT: Schenzle, Andreas J.
APPIICANT: No. US20020102699Alton,
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                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Methylomonas 16a
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CANT: Cheng, Qiong
OF INVENTION: Genes Involved in Isoprenoid Compounds Production
REFERENCE: CL1646 US NA
                                                                                                           285;
 61 NPISGVPEQDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNR 120
                                                         1 MDYAAGWGERWEAPAKLNLMLRITGRREDGYHLLQTVFQMLDLCDWLTFHEVDDGRVTLR
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Rouviere, Pierre
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Pred. No. 5.7e-156;
Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/934,868
CURRENT FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 81
SOPTWARE: Microsoft Office 97
SEQ ID NO 74
LENGTH: 285
TYPE: PRT
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                                                        Sequence 12, Application US/09941947A Publication No. US20030003528A1 GENERAL INFORMATION:
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Sequence 74, Application US/09934868
Patent No. US20020137190A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 285;
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APPLICANT: Brzostowicz, Patricia
APPLICANT: Cheng, Qiong
APPLICANT: DiCosimo, Deana J.
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APPLICANT: Schenzle, Andreas J
TITLE OF INVENTION: DENITRIFYING METHANOTROPHIC BACTERIAL STRAIN
FILE REFERENCE: CL1596 US NA
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APPLICANT: Odom, James M
APPLICANT: Schenzle, Andre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Methylomonas 16a
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Pred. No. 5.7e-156;
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CURRENT APPLICATION NUMBER: US/09/941,947A
CURRENT FILING DATE: 2001-09-01
PRIOR APPLICATION NUMBER: 60/229,907
PRIOR FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/229,858
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 60
SCFTWARE: Microsoft Office 97
SEC ID NO 12
                                                                                                                    ; SEQ ID NO 13766
; LENCTH: 279
; TYPE: PRT
; CRGANISM: Pseudomonas fluorescens
US-10-369-493-13766
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Query Match
Best Local Similarity
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Publication No. US20030233675A1
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APPLICANT:
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APPLICANT: Rouviere, Pierre E.
TITLE OF INVENTION: CAROTENOID PRODUCTION FROM A SINGLE CARBON SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            241 GACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSALYKKLEQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 NPISGVPEQDDLTVRAANILKSHTGCVRGVCIDIBKNLPMGGGLGGGSSDAATTLVVLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MDYAAGWGERWPAPAKINIMIRITGRRPDGYHLLQTVFQMLDLCDWLTEHEVDDGRVEUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LWGLGLSKRELMDLGLRLGADVFVFVFGCSAWGEGVSEDLQAITLFEQWFVIIKFDCHVN
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Odom, J. Martin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
42.1%; Score 638; DB 12;
49.6%; Pred. No. 1.2e-60;
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Pred. No. 5.7e-156;
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                DB 12;
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               Length 279;
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                                                                                                                                                                                                                                       IN PLANTS FOR PRODUCTION
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Matches 135;

Conservative

41;

Mismatches

0

Gaps

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RESULT 6
US-10-369-493-802
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LENGTH: 279
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 201, Application US/10369493 Publication No. US20030233675A1
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APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION ITILE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Kenorhabdus nematophilus -10-369-493-201
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PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10.0%; Score 620; DB 12; al Similarity 48.0%; Pred. No. 1.1e-58; 132; Conservative 36; Mismatches 101;
                                                                                                                                                                                                                                                                                                       125
                                                                                                                                                                                                                                                                                                                                                  125 GLSKRELMDLGLRLGADVEVEVEGCSAMGEGVSEDLQAITLEEQWEVIIKEDCHVNTGEI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 RNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYABARLTGTGACVFAQFCNK 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 MDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAENLT 191
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                                                                                                                                                 FAQFCNKEDAESALEGLKDRWLVFLAKGLNQSALY 279
                                                                                                                                                                                                    FTDPELKRNSPIRTLPALLQAPFKNDCEPIARKRFREVEQLLSWLLEYTPSRLTGTGACV 244
                                                                                                                                                                                                                                                    FSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACV
                                                                                                                                                                                                                                                                                                                                                                                                  NLIVRAARLLQDHAEKQSTGTQYRGADIHIHKRLPMGGGLGGGSSNAATVLIALNYHWQT 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPSPAKLNLFLYITGRRSDGYHELQTLFQFLDYGDEITITPRQDNQIRLLTPVKGVPNDD 64
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                                                                                                   FGEFESPASARKVINQAPEWMQGFVARGVNISPIH 279
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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
PILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 21079
LENGTH: 280
TYPE: PRI
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
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; ORGANISM: Escherichia coli
US-10-369-493-802
                                                                                                                                            ; ORGANISM: Xenorhabdus nematophilus US-10-369-493-21079
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     Query Match
Best Local Similarity
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Publication No. US20030233675A1
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Best Local Similarity 47.9%; Pred. No. 3e-58;
Matches 135; Conservative 39; Mismatches 96; Indels 1
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LENGTH: 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      242 ACVFAQFCNKEDAESALEGIKDRWI-VFLAKGINQSALYKKI 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70
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     38.6%;
Score 584.5; DB 12; Pred. No. 7.8e-55;
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LENGTH: 294
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Chen, Xianfeng TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE: 38-10(52052)B CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-369-493-15324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 47374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Xanthomonas campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
  257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LGLSKRELMDLGLRLGADVPVFVFGCSAMGEGVSEDLQAITLFEQWFVIIKFDCHVNTGE 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DLTVRAANLLKSH-----TGCVR-GVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWG 123
ATRAAAEQAMAHLPGNLRAWVVEGAAHSPLLDALD 291
                                                                                                                                                                 TLAELGLRLGADVPVFVRGHNAWAEGVGEKLTPISLPQAAYVLVDPGIHVPTPVLFQSQE 196
                                                                                                                                                                                                                                                    DDLMVRAARALQIHAGTALGAELRVDKRIPAGGGFGGGSSDAATVLVALNALWGLGLFVD 136
                                                                                                                                                                                                                                                                                           DDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR 129
                                                                                                                                                                                                                                                                                                                                     WPAPAKLNIFIQIVGRRADGYHLLQIVFRLIDWGDTVHVRLRTDGQIQRIGASLPGVAED 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VFAQFCNKEDAESALEGIKDRWIVFLAKGLNQSALY 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NLIVRAARLIQDHULQNNNKGTQHLGADIHIDKCLPMGGGLGGGSSNAATVLIALNYHWQ 124
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                                        CNKEDAESALEGIKDRWLVFLAKGLNQSALYKKLE 283
                                                                                                                         LTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAI-DALLCYAEARLTGTGACVFAQF 248
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                                                                                   LTRDAAPAKIADFASGSLLDNAFEPVLRRREPAIEAVFQALSRIGTPRLTGSGSGCFVEF
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                                                                                                                                                                                                                                                                                                                                                                                                                    38.5%; Score 584; DB
45.8%; Pred. No. 9.5e
tive 42; Mismatches
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9.5e-55;
ches 105;
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RESULT

38.4%;

Score 582;

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12;

Length 276;

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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FULE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
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US-10-369-493-16082
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; ORGANISM: Xanthomonas
US-10-369-493-16082
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SEQ ID NO 15690
LENGTH: 276
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16082, Application US/10369493
Pathlication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
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                                                              SEQ ID NO 16082
LENGTH: 276
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Publication No. US20030233675A1
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OP INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION INTILE OP INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10 (52052).B
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CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNKEDAESALEGIKDRWIVFLAKGINQSALYKKI 282
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46.0%; Pred. No. 1.4e-54;
tive 41; Mismatches 105;
                    campestris
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CURRENT APPLICATION NUMBER: US/10/369,493; CURRENT FILING DATE: 2003-02-28; PRIOR APPLICATION NUMBER: US 60/360,039; PRIOR FILING DATE: 2002-02-21; NUMBER OF SEQ ID NOS: 47374; SEQ ID NO 17551; LENGTH: 298; TYPE: PRT ORGANISM: Xylella fastidiosa
US-10-369-493-17751
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US-10-369-493-17751
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 17751, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 132; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES FILE REFERENCE; 38-10(52052)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cao,
APPLICANT: Hinh
APPLICANT: Slat
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                                                                                                                                                                           130 ALWHTRLDVAVLAALGLRLGADVPVFVHGCNAWAEGVGECLTEMILFGAAYLLLDPGVCV
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                                                                                                                                                                                                                                                               70 GESVTGVVEADDLVVRAAYLLKYATNVHLGADIFVEKRIPVGGGFGGGSSDAATVLLVLN 129
                                                                                                                                                                                                                                                                                                                                                      11 VDDGVGW-SAWPAPAKLNLFLQITGRRVDGYHELQTVFRLLDWGDTIHLRVREDGQIHRI 69
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                                                                                                                                                                                                                     RLWGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hinkle, Gregory J. Slater, Steven C. Soldman, Barry S. Chen, Xianfeng
                                                                                                                              NTGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSE-VVCKLYRPVKDAIDALLCYAEARLT 238
GSGSGCFVEFSTRDEAECALERLPYGLCAWVADGASRSPLLDVLK 294
                                          GTGACVFAQFCNKEDAESALEGIKDRWLVFLAKGINQSALYKKIE 283
                                                                                      PTRELFLDPDLTRDAS PATIGDF IAGTAFGNAFEPVLRRRESAVAGALDVLSEVGFARVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATRAAAEQAMAHLPGNLRAWVVEGAAHSPLLDAL 276
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Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                            44; Mismatches 106; Indels
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41; Mismatches 105;
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GENERAL INFORMATION:

APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Satter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/60,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR OF SEQ ID NOS: 47374
SEQ ID NO 9184
LENGTH: 270
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; ORGANISM: Xylella fastidiosa
US-10-369-493-9359
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-369-493-9184
                                                               APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
PILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US/003-02-28
PRIOR APPLICATION NUMBER: US/003-02-02
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 9359
LENGTH: 270
TYCH: DET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9359, Application US/10369493 Publication No. US20030233675A1 GENERAL INFORMATION:
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Publication No. US20030233675A1
                                                    TYPE: PRT
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ilarity 47.4%;
Conservative 4
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t; Pred. No. 1.7e-53;
42; Mismatches 98;
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Best Local Similarity

Query Match

Length 270;

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APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
PILE REFERENCE: 38-10(52052)B
CURRENT FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 19675
LENGTH: 213
RBSULT 15
US-10-369-493-8419
, Sequence 8419, Application US/10369493
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US-10-369-493-19675
; Sequence 19675, Application US/10369493
; Publication No. US20030233675A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 36.7%; Score 556; DB 12; Best Local Similarity 51.6%; Pred. No. 6.6e-52; Matches 110; Conservative 34; Mismatches 67
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                                                                                                                     181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 STRDEAECALERLPYGLCAWVADGASRSPL 270
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                                                                                                                                                                                                            RLMALGLELGADVPVFIYGRNAFABGVGEELHAVDLPSAWYVVLTPPVQISTAAVFTSKE 180
                                                                                                                                                                                                                                                                                                  DLCVRAAKLIRQRFGRESLGVKIHLEKNIPLGGGLGGGSSDAATTLIALNRIWGINWKRE 120
                                                                                                                                                                                                                                                                                                                                 DLTVRAANLLKSHTGCVR-GVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLMGLGLSKR 129
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                                                                                                                   LTRNTIPIKMAAFSMGQGHNDLEPVAMRM-QPV
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Pred. No. 1.7e-53;
2; Mismatches 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052)B
FILE REFERENCE: 38-10(52052)B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-2B
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
PRIOR FILING DATE: 2002-02-21
SEQ ID NO 8419
LENGTH: 233
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slatter, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                 113
  182
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                                                                                                                                                                                     62 TTÍLALNRÍNGVNÍ PREELMRIGÍSÍGADV ÞVFVFGQNAFAEGVG EELTPVALPDSNFVV 121
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                                            ALLCYA-EARLTGTGACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSAL 278
                                                                                                                                                                                                                                                                         DDGVIRVETDIPGVPADTDLVVRAARAMQAASGTVFGVDIAIDKILPMGGGIGGGSSDAA
WIKNYSPHARMIGSGACVFARFEDEQTAQRVMERLPSEWDGRCVKSISHHPI 233
                                                                                                                                                                                                           TTLVVLKRLMGLGLSKRELMDIGLRLGADVPVFVFGCSAMGEGVSSDLQAITLPEQMFVI
                                                                                          IHPROHVETAAIFSDERLIRNSPISIVADFAACTNKFAFGRNDLETIATAKFGEVARALE
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                      35.2%; Score 533; DB 12;
49.1%; Pred. No. 2.4e-49;
tive 35; Mismatches 77
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 233;
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Search completed: January 29, Job time: 20.4547 secs 2004, 16:21:17

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
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             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: pir1:*
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                                                                                                         GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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2 G81732 2 B81333 2 B86939 2 A870379 2 A874470 2 B71470 2 H72261 2 H86609 2 C81314 2 F71820 2 D82871 2 F82563 3 C64700 2 D64700 2
081732 871333 886939 A70379 A87115 H71261 B71470 H86609 C81314 D8711 D871820 D8711 D82583 C64700 C64700 T649047 F849047 F849047 F849047 F849047 F849047 F849047

ALIGNMENTS

RESULT 2
AH0245
probable 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.-) [imported]
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001

Yers

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conserved hypothetical protein 2 - Salmonella typhimurium C;Species: Salmonella typhimurium C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change C;Accession: S27732 R;Post, D.A.; Hore-Jensen, B.: Switzer
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R;Parkhill, J:; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, R;Parkhill, M.; Rw.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, deno-Tarraga, A.M.; Chillingworth, T.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, M.; Rutherford, M.; Stevens, R.; Whitehead, S.; Barrell, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford, M.; Rutherford,
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A; Residues: 1-283 < POS >
A; Cross-references: EMBL:M77236; NID:g154280; PIDN:AAA27195.1;
A; Cross-references: EMBL:M77236; Drotein HP1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Post, D.A.; Hore-Jensen, B.; Switzer, R.L.
submitted to the EMBL Data Library, October 1991
A;Description: The prs gene of E. coli and S. ty,
A;Reference number: S27568
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A;Cross-references: GB:AL590842;
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A; Residues: 1-299 < KI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Accession: S27732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
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Best Local Similarity
Matches 140; Conserv
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                                         GLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEI 184
                                                                                                                         DLTVRAANLL---KSHTGCV---RGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGL 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DPELKRNTPIRPLAALLSTPYANDCEPIARKRFREVEQALSWLLEYAPSRLTGTGACVFA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDLTVRAANLLKSHTG---CVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGL 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RWPAPAKLNIMIRITGRRPDGYHLLQTVPQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ 69
   GLSIDELATLGLTLGADVPVFVRGHAAFAEGVGEILTPVNPPEKMYLVAHPGVSIPTPVI
                                                                                                                                                                                                                                                            WPSPAKLNLFLYITGQRADGYHTLQTLFQFLDYGDTLHIBPRHDGEIHLLTPVNGVENED
                                                                                                                                                                                                                                                                                                                       WPAPAKLNIMIRITGRREDGYHLLQTVFQMLDLCDWLTEHPVDDGRVTLRNPISGVPEQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EFDTESSARQVL-SIAPEWLHGFVARGVNVSPLHR 287
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Pred. No. 3e-51;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         Score 629; DB 2;
Pred. No. 3.7e-49;
5; Mismatches 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 283
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Nature 413, 848-852, 2001
A;Auchors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.;
A;Title: Complete genome sequence of a multiple drug resistant
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0720
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C;Keywords: phosphotransferase
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A; Residues: 1-283 < PAR>
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Best Local
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                                                                                                                                                                                                         GLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGBI
                                                                                                                                                                                                                                                        NLIVRAARLLMKVASESGRLPAGSGADISIEKRLPMGGGLGGGSSNAATVLVALMHLWQC
                                                                                                                                                                                                                                                                                              DLTVRAANLL---KSHTGCV---RGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGL
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                                                                                                                                                                                                                                                                                                                                                                                WPAPAKLNLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQD
FARFDTESCARQVLEQAPE-WLNAFVAKGVNLSPLHREL 282
                                        FAQFCNKEDABSALEGLKDRWL-VFLAKGLNQSALYKKL 282
                                                                                                                        FSAENLTRNSAVVIMSDFLAGDHRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACV
                                                                                                                                                                     GLSIDELATIGITIGADVPVFVRGHAAFAEGVGEILTPVNPPEKWYLVAHPGVSIPTPVI
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                                                                                FKDPQLPRNTPKRSIDTLLKCEFSNDCEVIARKRFREVDAALSWILLEYAPSRLTGTGACV
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                                                                                                                                                                                                                                                                                                                                                                                                                         Score 629; DB 2;
Pred. No. 3.7e-49;
5; Mismatches 96
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Davis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HP1443
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                                                                                                                                                                                                                                                                                                                                                                                                                             96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 283
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Salmonella enterica serov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         D.; Wain, J.; Churcher,
, L.; White, N.; Farrar,
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; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Raj Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81875
A;Status: preliminary
A;Molecule type: DNA

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.;

S.D.; Chu; Mungall,

Churcher,

urcher, C.; Klee, K.; Quail, M.A.;

S.R.; Morel Rajandream,

Z2491

C; Accession:

A81875

hypothetical protein NMA1092 [imported] - Neisseria meningitidis (strain Z2491 serogroup C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001

A81875

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R;Hayashi, T.; .....gasawara, N.; Yasunaga, Pasawara, N.; Yasunaga, 2001
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A;Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84355.1; PID:g737978
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
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C; Superfamily:
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A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: NMA1092
C; Superfamily:
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A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: A90843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ychB protein [similarity] - Escherichia coli (strain O157:H7, substrain RIMD O5C;Species: Escherichia coli (c;Species: Escherichia coli (c;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001 C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 02-Nov-2001 C;Accession: A90843 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Basawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-283 <HAY>
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                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69 QDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSK 128
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 PVIFKDPELPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
                                   GEIFSAENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTG
                                                                                               WGLGLSKRELADLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVVIIKPDCHVNT
                                                                                                                                                                   DDLTVRAANLL-----KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRL 121
                                                                                                                                                                                                                     QWPSPAKLNLFLYITGQRADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPYEGVEHE
                                                                                                                                                                                                                                                       RWPAPAKIMIMIRITGRRPDGYHLLQTVFQMIDLCDWLTFHPVDDGRVTLRNPISGVPEQ 69
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                                                                                                                                               DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
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                                                                      WQCGLSMDELAEMGLTLGADVPVFVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
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                                                                                                                                                                                                                                                                                                             Score 616; DB 2;
Pred. No. 5.5e-48;
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Pred. No. 9.3e-49;
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A; Residues: 1-283 <BLAT>
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Best Local
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 122
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A;Cross-references: EMBL:U18555; NID:g968925; PIDN:AAC43434.1; PID:g968927
A;Experimental source: strain K-12
R;Blattner, F.R.; Plunkett III, G.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: E64867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene 121, 127-132, 1992
A;Title: Cloning and characterization of genes involved A;Reference number: JC1381; MUID:93051347; PMID:1427085
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R;Strohmaier, H.; Remler, P.; Renner, W.; Hogenauer, G.
J. Bacteriol. 177, 4488-4500, 1995
A;Title: Expression of genes kdsA and kdsB involved in 3-deoxy-D-manno-octulosonic acid anscriptional level in Escherichia coli K-12.
A;Reference number: I60364; MUID:95362678; PMID:7543480
A;Accession: I83566
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A;Map position: 26 min
C;Superfamily: conserved hypothetical protein
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R;Post, D.A.; Hove-Jensen, B.; Switzer, R.L.
J. Gen. Microbiol. 139, 259-266, 193
A;Title: Characterization of the hemA-prs region of the A;Reference number: A47706; MUID:93171869; PMID:7679718
A;Accession: B47706
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A;Residues: 'M',61-207,'TQAYGRANTKGAPFRRTAVKCRSLGKLLLECAGKCLLRVEAVLQRDVQNRTRSQA'
A;Cross-references: DDBJ:D10264; NID:9216522; PIDN:BAA01106.1; PID:9912433
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A;Residues: 1-283 <POS
A;Cross-references: EMBL.M77237; NID:g147380; PIDN:AAA24434.1; PID:g147382
A;Experimental source: strain K-12
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                                                     WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNT 181
                                                                                                                                                        DDLTVRAANLL------KSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTEVVLNRL 121
                                                                                                                                                                                                                                               QWPSPAKLNIFLYITGQRADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPVEGVEHE 63
                                                                                                                                                                                                                                                                                                       RWPAPAKLNIMIRITGRRPDGYHLIQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ 69
WQCGLSMDELAEMGLTLGADVPVFVRGHAAFAEGVGEILTPVDPPEKWYLVAHPGVSIPT
                                                                                                                       DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
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; Pred. No. 5.5e-48;
39; Mismatches 96
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A; rettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R. A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A; Raccession: B81149

A; Status: preliminary A; Molecule type: DNA
                                                                                                                                                                       conserved hypothetical protein NMB0874 [imported] - Neisseria meningitidis (strain C;Specles: Neisseria meningitidis (C;Specles: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001 C;Accession: B81149 R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen
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A; Residues: 1-295 < HEI>
A; Cross-references: GB: AE004289;
A; Cross-references: serogroup
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Nature 406, 477-483, 2000
A; Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A; Reference number: A82035; MUID:20406833; PMID:10952301
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C; Superfamily: conserved hypothetical protein HP1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 C;Accession: E82109
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTEHPVDDGRVTLRNPISGVPEQD
                                                                                                                                                                                                                                                                                                                                         RKDAQAVFAQLSDNVLAFVAQGRNVSPLRKTL
                                                                                                                                                                                                                                                                                                                                                                        KEDAESALEGIKDRWEVFLAKGINQSALYKKI 282
                                                                                                                                                                                                                                                                                                                                                                                                              MRNTPKRDLASLLTTPYENDCEKIVRSLYPEVDKQLSWLLQYAPSRLTGTGSCVFAEFSS 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACVFAQFCN 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAEIGLALGADVPVFTRGFAAPAEGVGEELSAVEPEEKWYLVVRPAVSIATKDIFTHPQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAENL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NLIYKAAMALKNAAQSPLGADIQLHKVLPMGGGIGGGSSNAATTLVALNYLWQTGLSDDQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPSPAKLNLFLYITGRRANGYHDLQTLFQFLDHGDELTITANNSGNITLSPALADVALED
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47.1%; Pred. No. 5.8e-48;
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O1; strain N16961; biotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                           284
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                                                                                Rappuoli, R.; strain MC58.
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C;Superfamily
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A; Molecule type: DNA
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Best Local Similarity
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A;Residues: 1-281 <TET>
A;Cross-references: GB:AE002439; GB:AE002098; N:A;Cross-references: GB:COURT B, strain MC58
C;Genetics:
A;Gene: NMB0874
C;Superfamily: conserved hypothetical protein HI
                                                                                                                                                                                                                           LWGLGLSKREIMDLGLRLGADVEVFVEGCSAWGEGVSEDLQAITLPEQWEVIIKPDCHVN
                                                                                                                                                                                                                                                                                               NPVDGMPQEVDLSYRAASLLQXYARNPAGVEIWLDXXIPTGAGLGGGSSDAATVLLVLNR
                                            LIGIGACVFAQFCNKEDAESALEGLKDRWLVFLAKGLNQSAL
                                                                                                                                                                                                   WWQCGLTQRQLIDSGAALGADVPFFIPGKNAFARGIGDRLDEMDIPKQWYVIVKPPVHVS
                                                                                                                                                                                                                                                                                                                                               NPISGVPEQDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MDYAAGWGERWPAPAKINIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLR 60
MTGSGACVFTACQDRNSAYNIYRQVSDLYBAYLAEGLSKHPL 278
                                                                                                                                                                                                                                                                                                                                                                                                 MNIADG-RQAFSAPAKLNLDLRITGRREDGYHNIESIFCLIDLQDTVYLKPRDDGKIILH
                                                                                               TAKIFTHESLTRNSASSIMPTF---QNLQPFRNDMQAVVFKEYPEVWKAYSELSRYGFAL
                                                                                                                                              TGEIFSAENLTRNSAVVTMSDFLAGDN----RNDCSEVVCKLYRPVKDAIDALLCYAEAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   53 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 615; DB 2;
Pred. No. 6.7e-48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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A;Residues: 1-283 <STO> A;Cross-references: GB:AB005174; NID:g12514921; PIDN:AAG56066.1; GSPDB:GN00145; A;Experimental source: strain O157:H7, substrain EDL933 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glass Iller, L.; Grotbeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, Iller, L. 2001 Nature 409, 529-533, 2001 A;Title: Genome sequence of enterohemorrhagic Escherichia co hypothetical protein ychB [imported] - Escherichia C;Species: Bscherichia coli C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 C;Accession: F85700 B.; Glasner, imalanta, E.; #text_change 14-Sep-2001 coli (strain 0157:H7, substrain Coli O157:H7 J.D.; Rose, Potamousis, D.J.; Mayhew Apodaca, UWGP: Z19 EDL93

conserved hypothetical protein HP1443

PVIFKDPSLPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG GET FSAENLTRNSAVVIMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTG WQCGLSMDELAEMGLTLGADVPVFVRGHAAFAEGVGBILTPVDPPEKWYLVAHPGVSIPT WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNT QWPSPAKLNLFLYITGQRADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPVEGVEHE RWPAPAKLNIMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNP1SGVPEQ DNLIVRAARLLMKTAADSGRLPTG--SGANISIDKRLPMXGGLGGGSSNAATVLVALNHL DDITTYRAANIL------KSHTGCVRGVCIDIEKNIPMGGGLGGGSSDAATTLVVLNRL 40.2%; Score 609; DB 2; 47.5%; Pred. No. 2.4e-47; tive 39; Mismatches 97 97; Length 283 Indels 12; Gaps 181 121 63 69 241 241 181 121 4

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Rifleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Schit, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; ABriones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, as-Neto, E.; Docena, C.; 31-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                    C;Accession: F82532
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Ni Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below A;Accession: F82532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein HI1608 - Haemophilus influenzae (strain Rd K C;Species: Haemophilus influenzae C;Species: Haemophilus influenzae C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 19-May-2000
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                                                                                           A;Residues: 1-298 <SIM>
A;Cross-references: GB:AE004071;
                                                                                                                                                                                                                                                                                                                                         C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Sep-2000
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A; Residues: 1-321 < TIGR >
                                                                                                                                         A; Molecule type: DNA
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENNLIYRAAKLIQEKANIQIGANIHIDKIIPMGGGVGGGSSNAATALVSINYIMQANISI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSK 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RWPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFH-PVDDGRVTLRNPISGVPB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACVFAQECNKEDAESALEGLKDRWL-VFLAKGLNQSALYKKL 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DHBABAQAVFRQKPBAFFGFVAKGLNVSPLHAMLKQ 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NLTRNSAVVIMSDFLAGDNRNDCSEVVCKLYREVKDAIDALLCYAEARLIGTGACVEAQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DELAKLGLTLGADVPIFVHGHAAFABGVGEKITYCEPAEKWFVILKPDDSISTAVIFQDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         conserved hypothetical protein HP1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.0%; Score 606.5; DB 2; 47.1%; Pred. No. 4.6e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45,
                                                                                             GB:AE003849; NID:g9107866; PIDN:AAF85442.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches 100:
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                                                                                                                                                                                                                                                                                                                                                                                            Xylella fastidiosa (strain
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A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme J.D.; Junqueira, M.L.; Kemper, B.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, B.E.; Laigre chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B.A.; Aluthors: Martins, B.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tsuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Ze A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
S49374
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-221 <TOU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein 2 - Pseudomonas aeruginosa (fragment)
C;Species: Pseudomonas aeruginosa
C;Date: 16-Peb-1995 #sequence_revision 01-Feb-1999 #text_change 26-M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: XF2645
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X82071; NID:g557256; PIDN:CAA57570.1; A;Experimental source: strain PAO1 C;Superfamily: conserved hypothetical protein HP1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: S49373
A; Accession: S49374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, A;Description: The Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Superfamily: conserved hypothetical protein HP1443
                                                                                                                                                                                                                                                                                       Query
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                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                       ocal Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     849374
                                                   NTGEIFSAENLTRNSAVVTMSDFLAGDNRNDCSE-VVCKLYRPVKDAIDALLCYAEARLT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ALWHTRLDVAVLAALGLRLGADVPVFVHGCNAWAEGVGECLTPMILPGAAYLLLDPGVCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RIWGLGLSKREIMDLGLRIGADVPVFVFGCSAWGBGVSEDLQAITLPEQWFVIIKPDCHV
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                                                                                       LTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKREL 131
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MDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAENLT 191
                                                                                                                                                                                                       PAPAKLNIMIRITGRRADGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPBQDD
                                                                                                                                                           PAPAKLNLFLHI1GRRDDGYHBLQTLFQFLDHGDBLHFEARQDGQVRLHTE1AGVPHDSN
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                                                                                                                                                                                                                                                                                    Score 551; DB 2
Pred. No. 3e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 580.5; DB 2
Pred. No. 9.4e-45;
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                                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                                                                                                 71;
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128

AALGÍRÍGADVÝVFTRGRAAFAEGVGEKÍTPVDIÝEPMYLVVVPQVLVSTAEIFSDPLLT 187

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A;Gene: ipk
                                                                         A;Molecule type: DNA
A;Residues: 1-299 <KUR>
A;Cross-references: GB:AE008688; PIDN:AAL41648.1; PID:g17738989; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutyavin, T.; Levy, R.; Li, M.; McClel; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, A;Authors: You, M.; Rightle, Y.; M.; Rightle, Y.; Perry, M.; Rightle, Y.; Perry, M.; Rightle, Y.; Perry, M.; Rightle, Y.; Perry, M.; Rightle, Y.; Perry, M.; Rightle, Y.; Perry, M.; Rightle, Y.; Perry, M.; Rightle, Y.; Perry,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein ipk [imported] - Agrobacterium tumefaciens (strain C58, C;Species: Agrobacterium tumefaciens C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Gene: ychB; BU170
C;Superfamily: cons
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A;Title: The Genome of the
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A;Molecule type: DNA
A;Residues: 1-294 <STO>
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A;Accession: G84949
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C;Species: Buchnera sp.
C;Apceles: Buchnera sp.
C;Apace: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: G84949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AP000398; GSPDB:GN00144
A;Experimental source: strain APS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Shigenobu, S.; Watanal
Nature 407, 81-86, 2000
                                                                                                                                                                                                                            ;Superfamily:
                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Accession: AB2654
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 QYTLKBLSLLGLRIGADVPGFVMGNTAVIEGIGDILYPIVQXEKWYLVVYPCINISTRYM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPAKINLELYVTGRRXDGYHNIQTLFQFLDYGDQFXIIANKTGNIELFTEKKIFMNVQNS 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FAQFCNKEDAESALEGIKDRWIVFLAKGINQSALYKKI 282
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSEFDNKKSAQKIFSVLPKNVQGFIAKSVNISPLHKTL 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .7e-37
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Best Local
                                                                       196
                                                                                                                                               136 AIAPEKLKSLALKIGADVPMCLASRPLIARGIGEDIBALTDLPELSMVLANPLKAVSTPE
                                                                                                                                                                                125 GLSKREIMDIGIRIGADVPVFVFGCSAWGEGVSEDIQAIT-LPEQWFVIIKPDCHVNTGE 183
                                                                                                                                                                                                                       76
                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                                                                             13 APAKLNLMLRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNP----ISGVPE 68
                                                                                                                                                                                                                                                                                                                                                                      99:
                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                       BA---RLTGTGA-C--VFAQFCNKEDAESALEGLKDRW 265
                                                                                                                                                                                                                     GDNLVTRARDILRDALASTGQPARPVDIHLEKNLPVASGIGGGSADAAATLRGLLRHWDA 135
                                                                       IFRRLQNKVNPHLPTPSTIGWATTGWMDFLA-QSRNDLQPPAQALL-PBIGEITGLLSEE 253
                                                                                                                                                                                                                                                         QDDLTVRAANLLK---SHTG-CVRGVCIDIBKNLPMGGGLGGGSSDAATTLVVLNRLWGL 124
                                                                                                                                                                                                                                                                                          APAKINLALHVTGQRADGYHLLETLVTFTAAGDMIRIRDAATDSFSISGPFGDLLSAGDS 75
GATLVRMSGSGATCFGIFHSFDAAKNAETSLRKKRPGW
                                                                                                            IFSAENLTRNSAVVTMS-----
                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                   21.6%; Score 327.5; DB 2; 35.6%; Pred. No. 6.8e-22;
                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                          -DFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYA 233
                                                                                                                                                                                                                                                                                                                                                                  ,111;
     291
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                                                                                                                                                                                                                                                                                                                                                                                                       Length 299;
                                                                                                                                                                                                                                                                                                                                                                      27;
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Search completed: January 29, 2004, 15:55:31 Job time: 9.38564 secs

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Result
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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      SwissProt_41:*
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Copyright (c) 1993 - 2004 Compugen Ltd
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28-FEB-2003 (Rel. 41, Last annotation update)
24-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC
4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kin
1SPE OR IPK OR RSC0396 OR RS03325.

Ralstonia solanacearum (Pseudomonas solanacearum).

Bacteria, Proteobacteria; Betaproteobacteria; Burkhol.
C Bacteria, Proteobacteria, Bataproteobacteria; Burkhol.
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HAMAP; MF_00061; -;
InterPro; IPR006204;
InterPro; IPR004424;
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InterPro, IPR004424; IspE.
Pfam; PF00288, GHMP_kinasee; 1.
TIGRFAMS; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis;
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NP_BIND 95
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                                                                                                                                                      PUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By similarity).

CAPALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-mettyl-D-erythritol.

PAYHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
                                                                    SIMILARITY: BELONGS TO THE ISPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192
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282 AA;
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Pred. No. 3.8e
36; Mismatches
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141EEBD4CF9438D3 CRC64;
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.8e-53;
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| kinase).
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Best Local S
Matches 140
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28-FEB-2003
28-FEB-2003
28-FEB-2003
                                         SEQUENCE FROM N.A.

STRAIN-CO-92 / Biovar Orientalis;

STRAIN-CO-92 / Biovar Orientalis;

MEDLINE-21470413; PubMed=11586360;

Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,

Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,

Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,

Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,

Peltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,

Lieather S., Moule S., Oyston P.C.F., Quail M., Rutherford K.,

Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;

"Genome sequence of Yersinia pestis, the causative agent of plague.

Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                   28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
28-FBB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cyvidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR IPK OR YPO2014 OR Y2293.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AMBL; AL646059; CAD13924.1; -.
HAMAP; MF 00061; -; 1.
InterPro; IPR006204; GHMP kinase.
InterPro; IPR004244; IspB.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMS; TIGR00154; ispB; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                         NCBI_TaxID=632;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    YERPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                        Enterobacteriaceae;
                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; Gammaproteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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NP_BIND 99
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                 SEQUENCE FROM
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N.A.
Biovar
                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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Pred. No. 7.3e-53;
"" ematches 93;
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                                                            plague. *;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 137
QBEARO;
[15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between
the Euro
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HAMAP; MF_00061; -; 1.

InterPro; IPR006204; GHMP kinase.

InterPro; IPR006424; IspE.

Iffam; PF00288; GHMP_kinases; 1.

TIGRFAMs; TIGR00154; ispE; 1.

Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew C
Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDomough K.A., Nilles M.L., Matson J.S., E
Perry R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ414151; CAC90828.1; EMBL; AE013832; AAM85852.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified
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J. Bacteriol. 184:4601-4611(2002).

-!- FUNCTION: Catalyzes the phosphorylation of the position group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By
                                                                                                                                                                       ISPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBD outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way ified and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         similarity)
CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-
erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE ISPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          methyl-D-erythritol.
PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
                                                                                                                                                                    NOTHS
                                                                                                                                                                                                                                                                                                                                                       247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DDLTVRAANLLKSHTG----CVRGVCIDIEKNLPMGGGLGGGGSSDAATTLVVLNRLWGLGL
                                                                                                                                                                                                                                                                                                      EFDTESSÄRQVÍ-SIAPEWIHGFVÁRGVNVSPÍHR
                                                                                                                                                                                                                                                                                                                                                                                                               DPELKRNTPIRPLAALLSTPYANDCEPIARKRFREVEQALSWLLEYAPSRLTGTGACVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AENLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYABARLTGTGACVFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SKREIMDIGIRIGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNIGEIFS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QNLIVRAAKMIQKHPGNTFVPRGADISIDKCLPMGGGLGGGSSNAATVLVALNILMQCGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RWPAPAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFHPVDDGRVTLRNPISGVPEQ
                                                                                                                                                                                                                                                                                                                                                         QFCNKEDAESALEGIKDRWL-VFLAKGLNQSALYK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TDEQLADIGITIGADVPVFVRGHAAFAEGIGEKLQPAEPVEKWYLVIHPGVNIPTPIIFS
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299 AA;
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                                                                                                                                                                 STANDARD;
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32675 MW;
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49.8%;
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Pred. No. 1e-51;
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; E86651DA68E0D658 CRC64;
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                                                                                                                                                                                                                                                                                                      287
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        (BC 2.7.1.148) kinase).
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RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Heidelberg J.F., Paulsen I.T., Welson K.E., Gaidos E.J., Nelson W.C.,
RA Head T.D., Elsen J.A., Scott J., Beaman M., Brinkac L., Daugherty S.,
RA Meyer T., Tsapin A., Scott J., Beaman M., Brinkac L., Daugherty S.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,
RA Madupu R., Peterson J.D., Umayam L.A., White O., Welf A.M.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Vamathevan J., Weidman J., Impraim M., Lee K., Berry K., Lee C.,
RA Nueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Meyer T., Saith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealson K.H., Fraser C.M.,
RA Schownella oneidensis.",
RA Meyer T., Tapin H., Stapin H., Stapin H., Stapin H., Fraser C.M.,
RA Mueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,
RA Meyer T., Tapin H., Stapin                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AB015816; AAN56813.1; -.
TIGR; S03836; -.
Fiam; PF00066; -; 1.
Fiam; PF00288; GHMP kinases; 1.
TIGRFAMs; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/cr send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Complete proteome.
NP_BIND 98
SEQUENCE 284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shewanella oneidensis.
Bacteria; Proteobacteria; Gam
Alteromonadaceae; Shewanella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       step.
-i- SIMILARITY: BELONGS TO THE ISPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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  249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
SQQQALAALAKLPSDMQGFVAKGMNISPLIVRLNR
                                               NKEDAESALEGIKDRWIVFLAKGINOSALYKKIEQ
                                                                                                                               LTRNSAVVTMSDELAGDNRNDCSEVVCKLYR.PVKDAIDALLCYAEARLTGTGACVFAQFC
                                                                                                                                                                                               ELAAIGLKIGADIPVFIHGFAAFAQGVGERLQAVNPAELWYLVIAPDAHVSTAAVFQDPL
                                                                                                                                                                                                                                                                                                                                               DDLTVRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKR
                                                                                                                                                                                                                                                                                                                                                                                                      WPAPAKLNI-FLHINGRRSDGYHELQTLFQFVDCCDQLDFRVTDTPELILHSTMSAVVADS
                                                                                                                                                                                                                                                                                                                                                                                                                              WPAPAKLNIMIRITGRRPDGYHILQTVFQMLDLCDWLTFHPVDDGRVTLRNPISG-VPEQ
                                                                                                  LPRNTPKLGLDTLLSQPWANDCQELVVSKYPQVAKALGWLLEYAPSRMTGTGACVFGEFS
                                                                                                                                                                                                                                                    ELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAEN
                                                                                                                                                                                                                                                                                                 DNLILRAAKSLQQATGFNGGAEIWLDKRLFMGGGLGGGSSDAATTLVALNRLWNTQLSHD
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ilarity 49.1%;
Conservative 4
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30721 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 644.5; DB 1
Pred. No. 5.1e-51;
1; Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FE5A22B814242496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         284;
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Best Local S
Matches 133
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Rhee J.H., Kim :
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DABIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAMAP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatice Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                similarity).
-!- CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-SBP-2003 (Rel. 42, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase |
(4-dytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-2003
15-SEP-2003
15-SEP-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00288; GHMP kinases; 1.
TIGRFAMS; TIGR00154; ispE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Vibric vulnificus CMCP6.";
Submitted {DEC-2002} to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Catalyzes the phosphorylation of the position 2 hydroxy
group of 4-diphosphocytidyl-2C-methyl-D-erythritol {By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                         TIGRFAMs; TIGRO0154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE016797; AA008792.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: BELONGS TO THE ISPE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISPE OR WV10256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         methyl-D-erythritol. 
PATHWAY: Nonmevalonate terpenoid biosynthesis pathway;
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                               251
                                                              188
                                                                                              191
                                                                                                                            128
                                                                                                                                                                                         89
                                                                                                                                                                                                                     71 DITVRAANLIKSHTGCVRGVCIDIEKNIEMGGGLGGGSSDAATTIVVLNRIWGLGISKRE
                                                                                                                                                                                                                                                                                  11 WPAPAKLNIMIRITGRRPDGYHLLQTVFQMIDICDWLTFHPVDDGRVTLRNPISGVPEQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MF 00061;
                                                                                                                                                                                                                                                                                                                                 Similarity
                               KEDAESALEGIKDRWLVFLAKGINQSALYKKI 282
RSEAESILAQLSDNVSAFVAQGRNISPLKETL
                                                                                      TRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYAEARLTGTGACVFAQFCN
                                                                                                                          LADIGLKLGADVPVFVRGHAAPAEGVGEKLTPAQPEEKWYLVVRPDVHIATVDIFTHPQL
                                                                                                                                                          LMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPEQWFVIIKPDCHVNTGEIFSAENL
                                                              TRNTPKRSLETLLDSEYGNDCEKIVRMIHPKVDKQLSWLLQYAPSRLTGTGSCVFAEFNS
                                                                                                                                                                                       NLTWKAANALQKKTGCTLGANIHLNKILPMGGGIGGGSSNAATALVALNFLWQLGLSDDE
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                                                                                                                                                                                                                                                                                                                                                                              290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 42, Created)
(Rel. 42, Last sequence update)
(Rel. 42, Last annotation updat
                                                                                                                                                                                                                                                                                                                  Conservative
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31657 MW;
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                                                                                                                                                                                                                                                                                                                43;
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                                                                                                                                                                                                                                                                                                                Score 642; DB
Pred. No. 8.9e
43; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                            ATP (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                               8.9e-51;
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                                                                                                                                                                                                                                                                                                                  96;
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                                                                                                                                                                                                                                                                                                                                            Length 290;
                                                                                                                                                                                                                                                                                                                  Indels
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Q87RN7;
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15-SEP-2003
15-SEP-2003
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MSDLINE=22508454; PubMed=12620739;
Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";
Lancet 361743-749(2003).
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15-SEP-2003 (Rel. 42, Last sequence update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISEE OR VP0740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Complete proteome.
NP BIND 101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AP005075; BAC59003.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -
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Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio parahaemolyticus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transferase; Kinase; Isoprene biosynthesis; ATP-binding
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CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho-4-(cytidine                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methyl-D-erythritol.

PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
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132; Conser
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                     NKEDAESALEGIKORWIVFLAKGINQSALYKKIEQ
                                                                                                                                                                               LTRNSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYABARLTGTGACVFAQFC
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                                                                                                  LITRNIPKROLETILINAPSVNDCEKIVRMLYPEVDKQLSWLLQYAPSRLIGIGSCVFAEFS
                                                                                                                                                                                                                                                                ELAEIGLKLGADVÞVFVRGFSAFARGVGEKLSPANDEEKWYLVVRPNVSIATADIFRHPD
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48.0%;
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Pred. No. 3.2e-50;
""aratches 97;
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InterPro; IPR006204; GHMP_kinase.
InterPro; IPR004224; ISBE
Pfam; PF00288; GHMP_kinases; 1.
TIGRFAMs; TIGR00154; ispE; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as modified and this statement is not removed. It entities requires a license agreement (See htt or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Bacteriol. 185:2330-2337(2003).
-!- FUNCTION: Catalyzes the phosphorylation of the position group of 4-diphosphocytidyl-2C-methyl-D-erythritol (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Ty2 / ATCC 700931;
MEDLINE=22531367; PubMed=12644504;
Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
"Comparative genomics of Salmonella enterica serovar Typhi strains and CT18.";
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28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR IPK OR STY1905 OR T1097.
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                                                                                                                                                                                               Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
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CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-
erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                          Bower S.G., Hove-Jensen B., Switzer R.L.;
"Structure of the gene encoding phosphoribosylpyrophosphate synthetase (prsA) in Salmonella typhimurium.";
J. Bacteriol. 170:3243-3248 (1988).
-!- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION.
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P30753;
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MCClelland M., Sanderson K.E., Spieth J., Clifton S.W.
MCClelland M., Sondollik S., Ali J., Dante M., Du F., Ho
Courtney L., Porwollik S., Ali J., Dante M., Grewal N.,
Leonard S., Nguyen C., Scott K., Holmes A., Grewal N.,
Ryan B., Sun H., Florea L., Miller W., Stoneking T., N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIINE-93171869; PubMed=7679718;
Post D.A., Howe-Jensen B., Switzer R.L.;
"Characterization of the hemA-prs region of the Escherichia coli
Salmonella typhimurium chromosomes: identification of two open
reading frames and implications for prs expression.";
J. Gen. Microbiol. 139:259-266(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148) (CMX)
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase).
ESPE OR IPK OR STM1779.
                                                                                                                                                                                                                                                                                                                                     Ryan B., Sun H., Florea L. Waterston R., Wilson R.K.;
                                                                                                                                                                                                                                       MEDLINE=88257047; PubMed=2838463;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
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                                                                         GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL SIMILARITY).
CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)
erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)
D-erythritol.
 step.
SIMILARITY: BELONGS TO THE ISPE
CAUTION: Ref. 2 sequence differs
frameshift in position 268.
                                                               PATHWAY:
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Matches 140
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NP_BIND 99

CONFLICT 252

SEQUENCE 283 AA;
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HAMAP; MF 00061; -; 1.
InterPro; IPR006204; GHMP_kinase
InterPro; IPR004244; IspE.
Pfam; PF00288; GHMP_kinases; 1.
TIGRFAMs; TIGR00154; ispE; 1.
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EMBL; AE008779; AAL20694.1; -.
EMBL; AL90488; -; NOT_ANNOTATED_CDS.
PIR; S27732; S27732.
STRAIN=Z2491 / Serogroup A / Serotype 4A;

MEDLINE=2022556; PubMed=10761919;

Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.,

Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,

Klee S.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd

Jagels K., Leather S., Moule S., Mungall K., Quail M.A.,

Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
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16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR NMA1092.
                                                                                                                                                                                                                                                                                                                                                                                                                 Neisseria meningitidis (serogroup A).
Bacteria; Proteobacteria; Betaproteobacteria;
Neisseriaceae; Neisseria.
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Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
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E33EAF956D12A5BD CRC64;
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InterPro; IPR006204; GHMP kinase.
InterPro; IPR004244; IspE.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMS; TIGR00154; ispE; 1.
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between
                                                                                                 TSPE_PASMU STANDARD; PRT; 295 AA.
15-783;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR PM0245.
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Nature 404:502-506(2000).

-i-FUNCTICK; CATALYZES THE PHOSPHORYLATION OF THE POSITION
GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL (BY
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PIR; A81875; A81875.
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CAPALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-CAPALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-perythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-perythritol
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46.7%; Pred. No. 3.
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Bacteria; Proteobacteria; Gan Pasteurellaceae; Pasteurella NCBI_TaxID=747;

Gammaproteobacteria;

Pasteurella multocida.

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Best Local
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                                                                                   Q8FT04;
15-SEP-2003
15-SEP-2003
15-SEP-2003
                                                  15-SEP-2003 (Rel. 42, Created)
15-SEP-2003 (Rel. 42, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2003 (Rel. 42, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
Escherichia coll vo.
Racteria, Proteobacteria;
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InterPro; IPR006204; GHMP kinase.
InterPro; IPR004244; ISpE.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMS; TIGR00154; ispE; 1.
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Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
-!- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION 2 HYDROXY GROUP OF 4-DIPHOSPHOCYTIDYL-2C-WETHYL-D-ERYTHRITOL (BY
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NP_BIND 108
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MEDLINE=21145866; PubMed=11248100;
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CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol.
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                                        OR C1666.
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33064 MW;
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        Gammaproteobacteria;
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9; Mismatches
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Pred. No. 3.9e-49;
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XX MEDINE-2388234; PubMed-12471157;

XX MEDINE-2388234; PubMed-12471157;

XX MEDINE-2388234; PubMed-12471157;

XX MEDINE-2388234; PubMed-12471157;

XX Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

XX Melch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,

XX Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

XX Mobley H.I.T., Donnenberg M.S., Blattner F.R.;

YExtensive mosaic structure revealed by the complete genome sequence

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Best Local :
                     1SPB ECOLI
224209;
01-MAR-1992
01-MAR-1992
28-FEB-2003
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
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HAMAP; MF_00061; -; 1.
Pfam; PF00288; GHMP_kinases; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGRFAMs; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIGREAMS; TIGROO154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          - !- SIMILARITY: BELONGS TO THE ISPE FAMILY.
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NCBI_TaxID=217992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QWPSPAKLMLFLYITGQRADGYHTLQTLFQFLDYGDTISIELRDDGDIRLLTPVEGVEHE
                                                                                                                                                                                                                                               ACVFAEFDTESEARQVLEQAPE-WLNGFVAKGVNLSPLHRAM
                                                                                                                                                                                                                                                                                           ACVFAQECNKEDAESALEGIKDRWI-VFLAKGINQSALYKKI
                                                                                                                                                                                                                                                                                                                                             PVIFKDPELPRNTPKRSIETLLKCEFSNDCEVIARKRFREVDAVLSWLLEYAPSRLTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNLIVRAARLLMKTAADSGRLSTG--SGANISIDKRLPMGGGLGGGSSNAATVLVALNHL
                  (Rel. 21, Created)
(Rel. 21, Last sequence update)
(Rel. 41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   283 AA;
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                                                                                                                        STANDARD;
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Pred. No. 8.4e-49;
0; Mismatches 95
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                          update)
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Ikemoto K.,
Kimura S.,
Mori H., Mc
   Oshima T., Aiba H., Baba T., Fi
Ikemoto K., Inada T., Itoh T.,
Kimura S., Kitagawa M., Makino
Mori H., Motomura K., Nakamura
                                                                                                                                                             STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
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Remler P.,
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Escherichia coli, and
                                                                                                                                                                                                                                                                     Remler P., Woisetschlaeger M., Strohmaier H.; Submitted (OCT-1995) to the EMBL/GenBank/DDBJ
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Luettgen H., Robdich F., Herz S., Mungsintaweekul J., Hecht S
Schuhr C.A., Fellermeier M., Sagner S., Zenk M.H., Bacher A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Escherichia.
                                                            MEDLINE=97061202; PubMed=8905232;
                                                                              STRAIN=K12;
                                                                                                                     Science
                                                                                                                                                                                                                                                                                                                                                           Ikemi M., Murakami K., Hashimoto M., Murooka Y., "Cloning and characterization of genes involved in of delta-aminolevulinic acid in Escherichia coli.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=K12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phosphorylates the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            enzymatic step.";
Proc. Natl. Acad. Sci. U.S.A. 96:13714-13719(1999)
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                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                Gene 121:127-132(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biosynthesis of terpenoids: YchB protein of Escherichia coli "Biosynthesis of terpenoids: YchB protein of Escherichia coli "Biosynthesis the 2-hydroxy group of 4-diphosphocytidyl-2C-methyl-D-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lange B.M.,
                                                                                                                     complete genome sequence nce 277:1453-1474(1997).
                                                                                                                                                  Shao Y.;
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 Baba T., Fujita K., H
, Itoh T., Kajihara M
M., Makino K., Masuda
, Nakamura Y., Nashim
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                                                                                                                                     Escherichia coli K-12.";
 a K., Hayashi K., Honjo A.,
Ihara M., Kanai K., Kashimoto K.,
Masuda S., Miki T., Mizobuchi K.,
Nashimoto H., Nishio Y., Saito N
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SEQÜENCE FROM N.A.
STRAIN-0157:H7 / RIMD 0509952;
MEDLINE=21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunag Kuhara S., Shiba T., Hattori M., Shinagawa H.;
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              HAMAP; MF 00061; -; 1.
InterPro; IPR006204; GBMP kinase.
InterPro; IPR0062424; ISpB.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMS; TIGR00154; ispB; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                              EMBL; AE000219; AAC74292.1; -.
EMBL; D90756; BAA35066.1; -.
EMBL; AE005338; AAC55066.1; -.
EMBL; AP002556; BAB35136.1; -.
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EMBL; AF179284; AAF13867.1; --
EMBL; AF216300; AAF29530.1; --
EMBL; AB037116; BAA94247.1; --
EMBL; M77237; AAA24434.1; --
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MEDLINE=21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D., Rose D.J., Mayhaw G.F., Evans P.S., Gregor J., Kirkpatrick H.A. Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L. Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.;

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"A 718-kb DNA sequence of the corresponding to the 12.7-28.
                                                                                                                                                                                                              PIR; A90843; A90843.
PIR; B47706; B47706.
                                                                                                                                                                                                                                                                                                                                                                   EMBL; D10264; BAA01106.1; ALT_FRAME
EMBL; U18555; AAC43434.1; -.
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RES. 8:11-22(2001).

FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION 2 HYDROXY GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL. PHOSPHORYLATES ISOPENTENL PHOSPHATE AT LOW RATES. ALSO ACTS ON ISOPENTENOL, AND, MUCH LESS EFFICIENTLY, DIMETHYLALLYL ALCOHOL. DIMETHYLALLYL MONOPHOSPHATE DOES NOT SERVE AS A SUBSTRATE.

MONOPHOSPHATE DOES NOT SERVE AS A SUBSTRATE.

CATALYTIC ACTIVITY: ATP + 4-(cytidine 5'-diphospho)-2-C-methyl-perythritol = ADP + 2-phospho-4-(cytidine 5'-diphospho-4-(cytidine 5'-diphosp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  monophosphate kinase.
CAUTION: REF.4 SEQUEN
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proteome
                                                                                                                                                                                 EG11294; ispE.
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Matches 135;
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STRAIN=B1 Tor N1696i / Serotype Ol;

STRAIN=B1 Tor N1696i / Serotype Ol;

MEDLINE=20406833; PubMed=10952301;

Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,

Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,

Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,

McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,

McDonald S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (4 (Cytidine-5'-diphospho)-2-C-methyl-D-erythritol ISPE OR VC2182.
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16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 406:477-483(2000).
-!- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POS-
GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ISPB_VIBCH
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                                                                                                                                                                                                                                                                                                              SIMILARITY)

CATALYTIC ACTIVITY: ATP + 4-(Cytidine 5'-diphospho)-2-C-methyl-perythritol = ADP + 2-phospho-4-(Cytidine 5'-diphospho)-2-C-methyl-
                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE ISPE FAMILY.
                                                                                                                                                                                                                                                                                   erythritol = ADP + 2-p;
D-erythritol.
PATHWAY: Nonmevalonate
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                                                                                                                                                                                                                                                                                       STRAIN=WC58 / Serogroup B;

MEDLINE=20175755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson Fisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J., Relson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K., Melson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Dodson T., Ciecko A., Parksey D.S., Blair E., Cittone H., Clark E., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vanathevan J., Cotton M.D., Utterback T.R., Khouri H., Qin H., Vanathevan J., Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L., Smith H.O., Praser C.M., Moxon E.R., Rappuoli R., Venter J.C., "Complete genome sequence of Neisseria meningitidis serogroup B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last amoutation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
ISPE OR NMB0874.
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Eacteria; Proteobacteria; Betaproteobacteria;
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Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
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InterPro; IPRO06204; GHMP kinase
InterPro; IPRO0424; IspB:
Pfam; PF00288; GHMP kinases; 1.
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SIMILARITY).
SIMILARITY . ATP + 4-(cytidine CATALYTIC ACTIVITY: ATP + 4-(cytidine catalytic) = ADP + 2-phospho-4-(cytidine cytidine                                                                                                                                          ence 287:1809-1815(2000).

FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION
GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL (BY
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISPE HAEIN
P45271;
STRAIN=Rd / KW20 / ATCC 51907;
MEDLINE=95350630; PubMedc7542800;
Fleischmann R.D., Adams M.D., White O., Clayton R.A.,
Fleischmann R.D., Jadams M.D., Tomb J.-F., Dougherty B.A.
Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A.
McKenney K., Sutton G., Fitzhugh W., Fields C.A., Go
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley
                                                                                                                                                                                                                                                                                                                                        01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
(4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAMAD; MF_00061; -; 1.
InterPro; IPR006204; GHMP_kinase.
InterPro; IPR006204; IspE.
Pfam; PF00288; GHMP_kinases; 1.
TIGRPAMS; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comentities requires a license agreement (See http://www.isb-sib.ch/an or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gam
Pasteurellaceae; Haemophilus.
                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           Haemophilus influenzae.
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PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; fourth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237
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Pred. No. 2.4e
53; Mismatches
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                                                  Clayton R.A., Kirkness
Dougherty B.A., Merrick
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lley J.M.,
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| kinase)
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                           Merrick
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Matches 130
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InterPro; IPR006204; GHMP kinase.
InterPro; IPR006242; ISBE.
InterPro; IPR00424; ISBE.
Pfam; PF00288; GHMP kinases; 1.
TIGRPAMs; TIGR00154; ispE; 1.
Transferase; Kinase; Isoprene biosynthesis; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Weiter J.C.; Phillips C.A., Spriggs T., Hedblom E., Cotton M. Utterback T.R., Harma M.C., Nguyen D.T., Saudek D.M., Brandon Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O. Wenter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Science 269:496-512(1995).
-i- FUNCTION: CATALYZES THE PHOSPHORYLATION OF THE POSITION GROUP OF 4-DIPHOSPHOCYTIDYL-2C-METHYL-D-ERYTHRITOL (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U32834; AAC23252.1; -. TIGR; HI1608; -.
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D-erythrito
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263
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130; Conserv
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DHEAEAQAVFRQKPSAFFGFVAKGLNVSPLHAMLKQ
                            CNKBDABSALEGIKDRWIVFLAKGINQSALYKKLEQ
                                                                                       NLTRNSAVVTMSDFLAGDNRNDCSEVVCKLYR PVKDAI DALLCYAEARLTGTGACVFAQF
                                                                                                                      DELAKIGITIGADVPIFVHGHAAFAEGVGEKITYCEPABKWFVIIKPDDSISTAVIFQDP
                                                                                                                                                                             ENNLIYRAAKLIQEKANIQLGANIHLDKILPMGGGVGGGSSNAATALVSLNYLWQANLSI
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ilarity 47.1%;
Conservative 4
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Pred. No. 1.
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Result
No.
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Q8earo shewanella
Q8dff6 vibrio vuln
Q8df04 escherichia
Q8df04 escherichia
Q8d246 wiggleswort
Q8e745 streptococc
Q8d240 streptococc
Q8d240 brucella su
Q8cqu6 staphylococ
Q8d1j1 synechococc
Q8d1j1 synechococc
Q8d1j1 synechococc
Q8d1j1 oryza sativ
Q8s2g0 oryza sativ
Q8fqz4 corynebacte
Q8ezm8 leptospira
Q9js86 chlamydia p
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11 WPAPAKINIMIRITGRRPDGYHLLQTVPQMLDLCDWLTFHPVDDGRVTLRNPISG-VPEQ 69	Query Match 42.5%; Score 644.5; DB 16; Length 284; Best Local Similarity 49.1%; Pred. No. 1.5e-52; Matches 135; Conservative 41; Mismatches 98; Indels 1; Gaps 1;	QBEARO PRELIMINARY; PRT; 284 AA. QBEARO; (JERNO; (JERNO; (JERNO; (JERNELrel. 23, Last sequence update) (JERNA; (JERNELrel. 23, Last sequence update) (JERNA; (JERNELrel. 23, Last sequence update) (JERNA; (JERNELrel. 23, Last sequence update) (JERNA; (JER

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01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidyl-2C-methyl-D-erythritol 2-phosphate
                                                                                                                                                                                                                                                                                                                                                                                                                        Rhee J.H.,
Choy H.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
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01-MAR-2003
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Q8D2K6;
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                                                                                                                                             Aksoy S.;
                                             flies, Wigglesworthia glossinidia.
Nat. Genet. 32:402-407(2002).
EMBL; AB063522; BAC24494.1; -.
                                                                                                                                                                                                                                                                                    Wigglesworthia brevipalpis.
Bacteria, Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Wigglesworthia.
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MEDLINE=23388234; PubMed=12471157;

Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J.,

Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,

Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
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Escherichia coli 06.
  SEQUENCE
                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=22297718; PubMed=12219091;
Akman L., Yamashita A., Watanabe H.,
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STRAIN=HEMSIG / Serotype III;
MEDLINE=22242508; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Ch
Glasek T., Zouine M., Couve E., Lalioui
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Bacteria; Firmicutes; Lactobacillales;
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; AL766844; CAD45794.1; -.
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283 AA; 31075 MW; D195DA&A84CCOPEO CRC64;
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Pred. No. 3.8e-40;
3; Mismatches 98
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Matches 85
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QBDS40;
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Putative isopentenyl monophosphate kinase.
IPK OR SMU.1996.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidyl-2C-methyl-D-erythritol kinase.
ISPE OR SAG0153.
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MEDILINE=22222988; PubMed=12200547;

MEDILINE=22222988; PubMed=12200547;

Method II., Masignani V., Cieslewicz M.J., Eisen J.A., Peterson S.

Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,

Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,

DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,

Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora

Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione

Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
                                                                                                                                                                                                                             QBDS40
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Bacteria; Firmicutes; Lactobacillales;
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35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MDLGLRLGADVEVFVFGCSAWGEGVSEDLQAI-TLEEQWFVIIKPDCHVNTGEIF---SA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APAKLNIMIRITGRRPDGYHLIQTVPQMLDLCDMITFHPVDDGRVTLRNPISGVPEQDDL
                                                                                                                                                                                                                                                                                                                                                                                                  GTGACVFAQFCNKEDABSALEGLK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSISRVDIDLLKSAILSSDYQLMVKSMGNSLEDITITKNPVISTIKERMLNSGADVALMT
                                                                                                                                                                                                                                                                                                                                                                    GSGPTVFSMCSTEKKADRVFNSMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENLTR----NSAVVTMSDFLAGDNRNDCSEVVCKLYRPVKDAIDALLCYA---EARLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAIGPKIGSDVPYCLGGGCSLVLGKGEIVKPLPTLRPCWIVLVKPDPGISTKSIPRDIDC 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVFKAADIIKNQYGINKGVHIRLEKSIPVCAGLGGGSTDAAATIRALNRLWNLOMDYDEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TV-RAANLLKSHTGCVRGVCIDIEKNILPMGGGLGGGSSDAATTLVVLNRLWGLGLSKREL 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APAKLNIGIÐIKGRCDDGYHBLAMIMVSIDLNDYVTISELKEDCIVIDSDSSKMPLNNDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSGPTVFSMCSTEKKADRVFNSMK
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                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 332; DB 16;
Pred. No. 4.8e-23;
58; Mismatches 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FC93843F69C2DC0D CRC64;
                                                                                                                                                                                                                                                                                                                                                                    270
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                                                                                                              update)
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RP SEQUENCE FROM N.A.

RP STRAIN=1330 / Biovar 1;

RX MEDLINE=22247741; PubMed=12271122;

RX MEDLINE=22247741; PubMed=12271122;

RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

RA Paulsen I.T., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,

RA Read T.D., Dodson R.J., Durkin A.S., Kolonay J.F., Madupu R.,

RA Daugherry S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,

RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,

RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,

RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,

RA Riedmuller S., Tindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,

"The Brucella suis genome reveals fundamental similarities between

"The Brucella suis genome reveals fundamental similarities between

animal and plant pathogens and symbionts.";
RESULT

QUESTION

PROSECUTION

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Best Local S
Matches 87
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SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
STRAIN-URA159 / ATCC 700610 / Serotype C;
STRAIN-URA159 / ATCC 700610 / Serotype C;
STRAIN-URA159 / ATCC 700610 / Serotype C;
MEDLINE=22295063; PubMed=12397186;
Ajdlc D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Ajdlc D., McShan W.M., McLaughlin R.E., Savic G., Chang J.,
Carson M.B., Primeaux C., Tian R., Kenton S., Jia H., Lin S.,
Carson M.B., Primeaux C., Tian R., White J., Roe B.A., Ferretti
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
Li S., Zhu H., Najar F., Lai H., White J., Roe B.A., Ferretti
Carson Sequence of Streptococcus mutans UR159, a cariogenic (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q8G2D0;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidy1-2C-methy1-D-erythritol kinase.
ISPE OR BR0394.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brucellaceae; Brucella.
NCBI_TaxID=29461;
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NCBI_TaxID=1309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria;
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EMBL; AE015023; AAN59600.1; -.
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         Complete proteome
E 299 AA; 31188
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282 AA;
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Pred. No. 5.2e-22;
57; Mismatches 102
         A9B88FF4157BF513 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299
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Matches 92
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Chen Z., Wen Y.;
Submitted (NOV-2002) to the
EMBL; AB016751; AA005930.1;
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STRAIN=ATCC 12228;
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Bacteria; Firmicutes; Bacil
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GSGPTVY 252
                                             GTGACVF 245
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01-MAR-2003
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01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (
                                                  MEDLINE=2220767; PubMed=12235376; Takami H., Takaki Y., Uchiyama I.; Takami H. Takaki Y., Uchiyama I.; "Genome sequence of Oceanobacillus iheyensis is Ridge and its unexpected adaptive capabilities
                                                                                                                                                                                                                                                 Oceanobacillus iheyensis.
Bacteria; Firmicutes; Bacillales; Oceanobacillus.
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                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-HTE831 / DSM 14371 / JCM 11309;
                                                                                                                                                                                                                                   NCBI_TaxID=182710;
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EMBL; AP005370; BAC08052.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=BP-1;
MEDLINE=22225144;
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3 11 AA; 33799 MW; 08DF8F2E7726F78A CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DAIDALLCYA--BARLTGTGACVFAQFCNKEDAESALEGLK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ELMDLGLRLGADVPVFVFGCSAWGEGVSE-----DLQAIT------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ELKEQFLAAGAIASMMSGSGPTVFAL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YRQEFAATYAQTPSEQEKARQEGGSAILLQAIQQHDIAFLAANLRNDLEKVVLPRYPLVA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKPDCHVNTGEIFSAENLTR---NSAV----VTMSDF--LAGDNRNDCSEVVCKLYRPVK
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(TrEMBLrel. 23, Last sequence update)
(TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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     30:3927-3935 (2002)
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; Pred. No. 3.9e-18;
37; Mismatches 111;
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sasaki T., Matsumoto T., Yan
"Oryza sativa (japonica cult
clone:P0003D09."
Submitted (FEB-2001) to the
EMBL; AP003221; BAB86428.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Putative 4-diphosphocytidyl-2-C-methyl-D-erythri tol kinase.
P0003D09.22.
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Eukaryota; Viridiplantae; Screptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gramene; Q8S2G0;
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InterPro; IPR004424; IspE.
Pfam; PF00288; GHMP kinases; 1.
TIGREAMs; TIGR00154; ispB; 1.
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LMDIGLRIGADVPVF----VFGCSANGEGVSEDIQ---AITLPEQWFVIIKPDCHVNTGE
                                                                       SPCKINVFLRITGKRPDGFHDLASLFHVISLGDTIKFSLSPSKSKDRLSTNVAGVPVDES 151
                                                                                                                                                                                                               APAKLNIMIRITGRRPDGYHLLQTVFQMLDLCDWLTFH-PVDDGRVTLRNPISGVP-EQD
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                                                                                                                        DLTVRAANILKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATTLVVLNRLWGLGLSKRE
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                                                                                                                                                                                                                                                                                                                                                                 401 AA;
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                                                                                                                                                                                                                                                                                                                                                                 43840 MW;
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                                                                                                                                                                                                                                                                                     18.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cultivar-group)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                             Score 274; DB 10;
Pred. No. 2.3e-17;
16; Mismatches 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 280; DB 16;
Pred. No. 3.8e-18;
0; Mismatches 110;
                                                                                                                                                                                                                                                                                                                                                                 23A259FF4DDCF320 CRC64;
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                                                                                                                                                                                                                                                                                                                 DB 10;
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                                                                                                                                                                                                                                                                     81;
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                                                                                                                                                                                                                                                                                                                 Length 401;
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RESULT
Q86514
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Best Local :
                                                                                                                                                                                                                                                                                Q8G6I4
Q8G6I4;
01-WAR-2003
01-WAR-2003
01-MAR-2003
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01-MAR-2003
01-MAR-2003
                                                                                                                                                                                 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, Cmk,
4-(cytidine-5'-diphospho)-2-C-methyl-D-erythritol kinase.
ISPE OR BL0656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The entire genomic sequence of Corynebacterium efficiens Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; APOU5217; BAC17783.1; -.
                                                       Bifidobacteriaceae; Bifidobacterium.
NCBI_TaxID=216816;
                                                                                                                                                          Bifidobacterium longum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
KAWATABAYASI Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.
Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio
Usuda Y., Sugimoto S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Corynebacterium efficiens.
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Corynebacterineae; Corynebacteriaceae; Corynebacterium.
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      SEQUENCE
                                                                                                                            Bacteria; Actinobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2003
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E 315 AA; 32871 MW;
      FROM N.A
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(Trambirel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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28.3%;
                                                                                                                            Actinobacteridae;
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Pred. No. 9.6e-13;
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Query Match
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Matches 77
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Best Local S
Matches 74
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Q8EZM8; Q1-MAR-2003 (TEMBErel. 23, Created)
01-MAR-2003 (TEMBErel. 23, Last sequence update)
01-MAR-2003 (TEMBErel. 23, Last annotation update)
4-diphosphocytidyl-2C-methyl-D-erythritol kinase (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22294977; PubMed=12381787; Schell M.A., Karmirantzou M., Snei B., Vilanova D., E Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley Pridmore R.D., Arigoni F.;
                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases EMBL; AB011537; AAN51022.1; .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002)
EMBL; AE014687; AANZ4478.1; -.
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                                                                                                                                                                                                                                                                                                                    Kinase; Transferase; Complete proteome.
SEQUENCE 297 AA; 33271 MW; 51AA1F018DAA7872 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                  LVVLNRL--WGLGLSKRELMDLGLRLGADVPVFVFGCSAWGEGVSEDLQAITLPE-QWFV
                                                                         YDQVSERGDIKNNILYKTFIKARSLFPB-
                                                                                                                  ISGVPEQDDLT-----VRAANLLKSHTGCVRGVCIDIEKNLPMGGGLGGGSSDAATT 114
                                                                                                                                                        SPAKINLGLEIPFKRLDGFHEIRSVFLKISWGDDIBIBPASNGVFELFSNNEIILEKRKL
                                                                                                                                                                                             APAKLNIMIRITGRREDGYHLLQTVFQMLDLCDWLTFHFVDDGRVTL------RNP
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--LLNFLFSWRPFFTSDEMFVLAAEIGSDVPFFLGEGHAFVTGKGEILEEIEVHHGQGIL
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                                                                                                                                                                                                                                      12.9%; Score 196; DB 16; 26.3%; Pred. No. 3.5e-10; tive 53; Mismatches 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 204.5;
; Pred. No. 6e-1
44; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Leptospiraceae; Leptospira.
                                                                           -LPGVKIHLTKRISPAGGLGGGSTNAAS-
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Database
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Maximum DB seq length: 2000000000
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1: \SIDS1\gcgdata\geneseq\geneseq-emb1/AA1980.DAT:*
2: \SIDS1\gcgdata\geneseq\geneseq-emb1/AA1981.DAT:*
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4: \SIDS1\gcgdata\geneseq\geneseq-emb1/AA1982.DAT:*
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12: \SIDS1\gcgdata\geneseq\geneseq-emb1/AA1997.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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534	534	537	537	537	537	806	806	806	Score
66.3	66.3	66.6	66.6	66.6	66.6	100.0	100.0	100.0	% Query Match
158	158	159	159	159	159	157	157	157	% Query Match Length
21	21	24	22	21	21	23	23	23	DB
AAB27151	AAB27150	ABP70685	AAG63811	AAB27149	AAB11373	AAU80329	AAE22305	ABG61583	Length DB ID
B. subtilis essent	H. influenzae esse	Escherichia coli 2	2-C-methyl-D-eryth	E. coli essential	E. coli YGBB prote	Methylomonas 16a O	Methylomonas 16a 2	High growth methan	Description

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434	434	943	410	434	102	96	199	160	160	174	161	158	248	240	176	223	399	352	406	409	259	239	231	240	231	161	120	191	157	160	174	170	159	159	159	
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ABB92639	AAG38717	144	8	AAG08216	77	ဋ	AAY35167	AAB80182	AAG92667	ABP65843	AAG39032	AAE31686	AAB70488	AAB18226	AAU50581	ABB93990	AAB27153	AAW20628	AAB27154	AAY11013	AAG27633	AAG27448	AAG27449	AAG15275	AAG15276	AAB27152	ABP02539	ABG18263	AB849155	ABU06061	ABP79612	ABG75686	ABP70688	ABP70687	ABP70686	
	Arabidopsis thalia	B	_	₽	co		Chlamydia pneumoni	Corynebacterium gl	C glutamicum prote	Bifidobacterium lo	Arabidopsis thalia	Rhodococcus erythr	Plasmodium falcipa	Plasmodium falcipa	Propionibacterium	Herbicidally activ	T. pallidum essent	H. pylori cytoplas	H. pylori essentia	H. pylori ORF hp7e	Ç				Arabidopsis thalia	Synechocystis esse		Novel human diagno	Listeria monocytog	N. meningitidis va	 gonorrhoe 	C-methyl-D-	C-methyl-D-	å	2C-methyl-D-erythr	

ALIGNMENTS

ABG61583 standard; Protein; 157 AA.

ABG61583;

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RESULT 1
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ID ABGG1583
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     WPI; 2002-452200/48
                                                                                                                                                                                                                                                                                                            01-SEP-2000; 2000US-229858P
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                                                                                                       Koffas M, Odom JM,
                                                                                                                                                                                                                                                                                                                                                                                                              28-AUG-2001; 2001WO-US26827.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methylomonas 16a.
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                                                                                                       Schenzle A;
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N-PSDB; ABK83262

New high growth methanotrophic bacterial strain, useful for producing single cell proteins, grows on a Cl carbon substrate, and comprises a functional gene encoding in Embden-Meyerhof carbon pathway

Claim 11; Page 142-143; 157pp; English.

present. The bacterial strain of the invention can be used as a denitrifying agent for the conversion of nitrate or nitrite to nitrous oxide with methane or methanol as a carbon source. It is also used in the production of biomass including proteins, carbohydrates and a wide variety of pigments (particularly for isoprenoid pigments for the purpose of generating animal feeds), in production of terpenoid and carotenoid compounds, useful as pigments and as monomers in polymeric materials and in production of texpolysaccharides at high levels. Sequences ABG61551-ABG61590 represent high growth methanotrophic bacterial strain proteins of the invention. NA. The bacterial strain is useful for the production of single cell protein and for the biotransformation of a nitrogen-containing compound, e.g. ammonia, nitrate, nitrite or nitrogen. It is also useful for the production of a feed product comprising a protein, carbohydrates and a pigment and for reducing oxygen demand, for removing nitrates and nitrites in methane-containing environments such as landfills, waste water treatment systems or anywhere that methane, oxygen and nitrates are The invention relates to a high growth methanotrophic bacterial strain, which grows on a C1 carbon substrate e.g. methans and methanol, and comprises a functional Embden-Meyerhof carbon flux pathway comprising a gene coding a pyrophosphate dependent phosphofrutokinase enzyme or a 16 RNA. The bacterial strain is useful for the production of single cell 168 the

Š 뭥 Ś B S Query Match Best Local Similarity 121 157; 61 61 1 MIRVGMGYDVHRENDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK 60 HFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAAD 120 LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157 LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157 MIRVGMGYÐVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK Conservative 100. .0%; Score 806; DB 23; 0 Mismatches Indels Length 0 Gaps 60

AAE22305 standard;

(first entry)

Methylomonas 16a 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase.

RESULT 2
AAE22305
ID AAE2
XX AAE2
AC AAE2
AC AAE2
AC AAE2
XX AAE2
AC AAE2
XX Meth
XX AGN
KW ANTI
CKW ANTI
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CKW A aquacuiture; anti-oxidant; Carotenoid; isopentenyl

01-SEP-2000; 2000US-229858P

Sequence 157 AA;

Protein;

isopentenyl pyrophosphate; antheraxanthin; astaxanthin; diet; steroid; flavour; fragrance; electro-optic application; 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase; IspF:

Methylomonas 16a

04-SEP-2001; 2001WO-US27420

01-SEP-2000; 2000US-229907P.

DU PONT DE NEMOURS & CO D)

Brzostowicz PC, Cheng Q Odom JM, Picataggio SK, , io Dicosimo DJ, Rouviere PB; Koffas Z

2002-351711/38.

Producing carotenoid compounds e.g. antheraxanthin and astaxanthin, by using microorganisms having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which metabolize single carbon

Claim 45; Page 118-119; 156pp; English.

encoding an enzyme in the carotenoid biosynthetic pathway, under the control of regulatory sequences, and contacting the host cell with carbon substrate to produce a carotenoid compound. The method is useful for producing carotenoid compounds such as antheraxanthin and astaxanthin, by using microorganism having a nucleic acid molecule encoding enzymes in the carotenoid biosynthetic pathway and which methoblise single carbon substrates. The carotenoids have potent anti-oxidant properties useful in diet, and aquaculture elements. The carotenoids are also useful as intermediates in the synthesis of steroids flavours and fragrances and compounds for potential electro-optic applications. The present sequence is Methylomonas 16a sp. 2C-methyl-d-erythritol 2,4-cyclodiphosphate The method comprises a transformed metabolising carotenoid compounds. suitable levels of isopentenyl pyrophosphate and a nucleic acid molecule encoding an enzyme in the carotenoid biosynthetic pathway "man openate on trol of regulatory possessions of the carotenoid biosynthetic pathway "man openate on trol of regulatory possessions of the carotenoid biosynthetic pathway "man openate on trol of regulatory possessions of the carotenoid biosynthetic pathway "man openate of the caroten synthase (IspF) enzyme used in the invention.

Sequence 157 Š

밁 S Matches Query Match Best Local 157; Similarity MIRVGMGYDVHRFNDGDHIIIGGVKIPYEKGLEAHSDGDVVLHALADAIIGAAALGDIGK 60 MIRVGMGYDVHRPNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK Conservative 100.0%; 0 Score 806; DB 23; Pred. No. 1.2e-87; Mismatches Indels 0 60 ٥,

121 121 LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157 LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER

62 61

HFPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAFK%LPHVFGMRANIAAD HEPOTOPNEKGADSRVLLRHVYGIVKEKGYKLVNADVTI IAQAPKMLPHVPGMRANIAAD

120

120

RESULT 3
AAUGO129
ID AAUG
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AAU80329 standard; Protein; 157

AAU80329;

15-JUL-2002 (first entry)

Methylomonas 16a ORFS ygbB/ispF protein sequence.

Isoprenoid biosynthetic enzyme; isoprenoid compound; feed additive; keratenoid; pigment; flavour; fragrance; open reading frame 5; ORF5; ygbB; 2C-methyl-d-erythritol 2,4-cyclodiphosphate synthase enzyme; ispF

Methylomonas

WO200220733-A2

14-MAR-2002.

29-AUG-2001; 2001WO-US26852

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RESULT 4
AAB11373
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Matches 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheng Q, Ku
Schenzle A,
      10-APR-1999;
                                                          10-APR-1999;
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                                                                                                                                                                                                                                 Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                      E. coli YGBB
                                                                                                                                                                                                                                                                                               YJES; KDTB; YQGF; YGGF; YHBC; YGBP; YGBB; YCHB; antibacterial; treatment; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new nucleic acid molecule encoding an isoprenoid biosynthetic enzyme isolated from Methylomonas 16a. The invention is useful for obtaining a nucleic acid molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ABK50085
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                                                                                                                                                                                                                                                                                                                                                                                                                                             22-FEB-2001
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A, Tomb J;
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                                                                                                                                                                                                                                                                                                                                                                                  protein.
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                                                          99DE-1016176.
      99DE-1016176
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Best Local 9
                                                                                                                                                                             Bacterial growth; inhibitor; ygbB; yfhC; yacE; ychB; yejD; yrfI; yggJ; yjeB; yiaO; yrdC; yhbC; ygbP; ybeY; gcpB; kdtB; pfs; ycaJ; b1808; yeaA; yagP; b1983; yidD; yceG; yjbC; antibacterial compound; H. influenza; S. pneumoniae; H. pylori; B. burgdorferi; pesticide; M. tuberculosis; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used to identify compounds that bind to the gene products, particularly in affinity selection assays. (II) and (IIa) are used to identify, or prepare, antibodies and other proteins that bind to the gene products. Substances that bind to (II) or (IIa) are potentially useful as entibacterials for treating a wide range of infections in humans and animals. Sequences antisense to (I) and (Ia) can also be used as antibacterials. The specified genes are widely distributed in bacteria but have no close homologs in eukaryotic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel Escherichia coli genes (I) encoding proteins (II) designated YQGF, YHBC, YGGJ, YGBP, YCHB, YGBB, YUBB and YDTB, and genes (Ia) that encode orthologous gene products (IIa) in other microorganisms and which have antibacterial activity. Recombinant microorganisms in which expression of (I) or (Ia) can be regulated activity and the microorganisms in which expression of (I) or (Ia) can be regulated activity.
                                                                               19-0CT-2000
                                                                                                                 WO200061793-A2
                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                E. coli essential protein ygbB
                                                                                                                                                                                                                                                                                                                  27-FEB-2001
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Labischinski H;
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Pred. No. 1.4e-55;
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09-APR-1999; 99EP-0107031 04-FEB-2000; 2000EP-0102111. 07-APR-2000; 2000WO-EP03135

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Matches 107
WPI; 2001-522353/57.
                          Seto H,
                                                                                           03-FEB-2000;
07-FEB-2000;
                                                                                                                                                                                                                                                         2-C-methyl-D-erythrytol-2,4-cyclodiphosphate synthetase; non-mevalonate pathway; 2-C-methyl-D-erythrytol-2,4-cyclodiphosphate; 2-phospho-4-(cytidine 5'-diphospho) 2-C-methyl-D-erythrytol; CDP-ME2P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to antagonists and inhibitors of 24 bacterial genes and proteins. The proteins are thought to be essential for growth in several species of bacteria (including S. pneumoniae, B. burgdorferi, H. influenza and H. pylori). The proteins and coding sequences shown in the specification can be used to identify antagonists and inhibitors which can be used in disease treatment and pesticides. In particular, they can be used against M. tuberculosis. The present sequence is one of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identifying antibacterial compounds, comprises identifying antagonist or inhibitor of the expression of a gene encoding polypeptide essential for bacterial growth or survival -
                                                                                                                                    25-JAN-2001; 2001WO-JP00483
                                                                                                                                                                                          WO200157223-A1
                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                               2-C-methyl-D-erythrytol-2,4-cyclodiphosphate synthetase
                                                                                                                                                                                                                                                                                                                                            29-0CT-2001
                                                                                                                                                                                                                                                                                                                                                                                                  AAG63811 standard; Protein; 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 4; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-687048/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Loferer H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GPCB-) GPC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                  SETO H.
KUZUYAMA T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRVGMGYDVHRENDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
                                                                                                                                                                                                                                            5'-monophosphate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MRIGHGPDVHAFGGEGPIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAALGDIGKL
                        Kuzuyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCHMDDVNVKATTTEKLGFTGRGEGIACEAVALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPDTDPAFKGADSRELLREAWRRIQAKGYTLGNVDVTIIAQAPKMLPHIPQMRVFIAEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FPDTDPNFKGADSRVELRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jacobi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BIOTECH
                                                                                           2000US-0180126.
2000JP-0029287.
                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                              isoprenoid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 537; DB 21;
Pred. No. 1.4e-55;
                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a 2-C-methyl-D-erythrycol-2,4-cyclodiphosphate synthetase. The enzyme is involved in the non-mevalonate pathway. It acts on 2-phospho-4-(cytidine 5'-diphospho) 2-C-methyl-D-erythrytol (CDP-ME2P). to produce 2-C-methyl-D-erythrytol-2,4-cyclodiphosphate and cytidine 5'-monophosphate. The enzyme has a molecular weight of 22 kDa, as determined by sodium dodecyl sulfate polyacrylamide gel electrophoresis. The enzyme or gene can be used to increase isoprenoid compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antibiotic; isoprenoid synthesis; crystal; (2C-methyl-D-erythritol 2,4-cyclodiphosphate Plasmodium falciparum; ispF.
                                                                             WPI; 2003-167170/16
N-PSDB; ABZ25497.
                                                                                                                                                        Bacher
                                                                                                                                                                                                          (PLAC )
                                                                                                                                                                                                                                                                                                                                                                13-MAY-2002; 2002WO-EP05238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABP70685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2-C-methyl-D-erythrytol-2,4-cyclodiphosphate synthetase, useful fo producing isoprenoids and for screening for non-mevalonate pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; AAH74788
                                                                                                                                                                                                                                                                                        15-MAY-2001;
25-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                       21-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200292800-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein co-ordinate data; herbicide; protozoacide; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABP70685;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibitors
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                                                                                                                                                                                                          MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
BACHER A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GCHMDDVNVKATTTEKLGFTGRGEGIACEAVALL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BTDVDFINVKATTTEKLGFBGRKEGIAVQAVVLI 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPDTDPNFKGADSRVLLRHVYGIVKEKGYKLVNADVTIIAQAPKMLPHVPGMRANIAADL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FPDTDPAFKGADSRELLREAWRRIQAKGYTLGNVDVT11AQAPKMLPH1PQMRVF1AEDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRIGHGFDVHAFGGEGPIIIGGVRIPYEKGLLAHSDGDVALHALTDALLGAAALGDIGKL
                                                                                                                                                     Hecht S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and also for screening for antibacterials.
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                                                                                                                                                                                                                                                                                        2001DE-1023597.
2001US-293875P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49pp; Japanese.
                                                                                                                                                           Huber
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Pred. No. 1.4e-55;
                                                                                                                                                        Kaiser J,
                                                                                                                                                           Rohdich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           malaria
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Novel crystal useful for identifying a potential inhibitor of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, compris

comprises

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RESULT
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Best Local Simi
Matches 107;
                                                                                                                                                                                                                                                                                                                               Bacterial growth; inhibitor; ygbB; yfhC; yacE; ychB; yejD; yrfI; yggJ; yjeE; yiaO; yrdC; yhbC; ygbP; ybeY; gcgE; kdtB; pfs; ycaJ; b1808; yeaA; yagF; b1983; yidD; yceG; yjbC; antibacterial compour H. influenza; S. pneumoniae; H. pylori; B. burgdorferi; pesticid M. tuberculosis; antibiotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to a crystal comprising 2C-methyl-p-erythritol 2,4-cyclodiphosphate synthase with or without zinc. The crystal is useful in an inhibitor-screening assay, and identified inhibitors are useful as antibiotics against bacteria or protozoa especially malarial parasite e.g. Plasmodium falciparum, and as herbicides. The inhibitors are also useful for inhibiting the synthesis of isoprenoids. The present sequence is 2C-methyl-p-erythritol 2,4-cyclodiphosphate synthase from Escherichia coli, encoded by the ispF
                                                                                                                                                                             09-APR-1999; 99EP-0107031.
04-FEB-2000; 2000EP-0102111.
                                                                                                                                                                                                                     07-APR-2000; 2000WO-EP03135
                                                                                                                                                                                                                                                   19-OCT-2000
                                                                                                                                                                                                                                                                             WO200061793-A2
                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB27150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB27150 standard;
           Disclosure;
                                   Identifying antibacterial compounds, comprises identifying antagonist or inhibitor of the expression of a gene encoding polypeptide essential for bacterial growth or survival -
                                                                                                                          Loferer
                                                                                                                                                   (GPCB-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                   influenzae essential protein ygbB
                                                                                            2000-687048/67.
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                                                                                                                                                   GPC
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                                                                                                                       Jacobi A:
                                                                                                                                                   BIOTECH
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          4; 75pp;
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          English
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Pred.
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No. 1.4e-55;
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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to antagonists and inhibitors of 24 bacterial genes and proteins. The proteins are thought to be essential for growth in several species of bacteria (including S. pneumoniae, B. burgdorferi, H. influenza and H. pylori). The proteins and coding sequences shown in the specification can be used to identify antagonists and inhibitors which can be used in disease treatment and pesticides. In particular, they can be used against M. tuberculosis. The present sequence is one of the proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                    Bacterial growth; inhibitor; ygbB; yfhC; yacE; ychB; yejD; yrfI; yggJ; yjeB; yiaO; yrdC; yhbC; ygbP; ybeY; gcpE; kdtB; pfs; ycaJ; bl1808; yeaA; yagF; bl983; yidD; yceG; yjbC; antibacterial compound; H. influenza; S. pneumoniae; H. pylori; B. burgdorferl; pesticide; M. tuberculosis; antibiotic.
                                                                                             Disclosure;
                                                                                                                      Identifying antibacterial compounds, comprises identifying an antagonist or inhibitor of the expression of a gene encoding polypeptide essential for bacterial growth or survival.
                                                                                                                                                                                                                                                               09-APR-1999;
04-FEB-2000;
                                                                                                                                                                                                                                                                                                         07-APR-2000;
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                                                                                                                                                                                                                                                                                                                                                                                           Eacillus subtilis.
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                                                                                                                                                                                                                                     GPC BIOTECH AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           158 AA;
                                                                                            Pig 4;
                                                                                                                                                                                                        Jacobi A;
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2000EP-0102111.
                                                                                                                                                                                                                                                                                                         2000WO-EP03135
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                                                                                            75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein ygbB
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Pred. No. 3.1e-55;
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The present invention relates to antagonists and inhibitors of 24 bacterial genes and proteins. The proteins are thought to be essential for growth in several species of bacteria (including 5. pneumoniae, B. burgdorferi, H. influenza and H. pylori). The proteins and coding sequences shown in the specification can be used to identify antagonist and inhibitors which can be used in disease treatment and pesticides.

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pesticides. In

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Best Local
 identified inhibitors are useful as antibiotics against bacteria or protozoa especially malarial parasite e.g. Plasmodium falciparum, as herbicides. The inhibitors are also useful for inhibiting the
                                  The present invention relates to a crystal comprising 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase with or without zinc. The crystal is useful in an inhibitor-screening assay, and
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein co-ordinate data; herbicide; protozoacide; antibacterial; antibiotic; isoprenoid synthesis; crystal; enzyme; 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase; malaria; Plasmodium falciparum; ispF; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        particular, they can be used against M. tuberculosis. The present sequence is one of the proteins of the invention.
                                                                                  Example 2; Page -; 214pp; English
                                                                                                                   Novel crystal useful for identifying a potential inhibitor of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, comprises 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase protein wit
                                                                                                                                                                                                                                                                                                                                                                          Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
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                                                                                                          without zinc
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                                                                                                                                                                                          Bacher A,
                                                                                                                                                                                                                                                      25-MAY-2001;
                                                                                                                                                                                                                                                              15-MAY-2001;
                                                                                                                                                                                                                                                                                      13-MAY-2002;
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BACHER A.
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2001US-293875P.
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                          antibiotic; isoprenoid 2C-methyl-D-erythritol Plasmodium falciparum;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   synthesis of isoprenoids. The present sequence is a mutant of 2C-methyl-D-crythritol 2,4-cyclodiphosphate synthase which was ger in an example from the invention.

Note: The present sequence is not shown in the specification, but derived from the wild-type sequence of Escherichia coli 2C-methyl-D-crythritol 2,4-cyclodiphosphate synthase (ABP70685).
                                                               Novel crystal useful for identifying a potential inhibitor 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, compr 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase proteins.
                                                                                                           WPI; 2003-167170/16.
                                                                                                                               Bacher A,
                                                                                                                                                                                   15-MAY-2001;
25-MAY-2001;
                                                                                                                                                                                                                                        21-NOV-2002
                                                                                                                                                                                                                                                                                             Misc-difference
                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                            Protein co-ordinate data; herbicide;
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                                                                                                                                                                                                                  13-MAY-2002;
                                                                                                                                                                                                                                                              WO200292800-A2
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2001US-293875P
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                                                                                                                               Huber
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                                                                                                                                                                                                                                                                                                                                                                      synthesis; crystal; enzyme;
2,4-cyclodiphosphate synthase; malaria;
                                                                                                                                                                                                                                                                                   "Wild-type His
                                                                                                                                                                                                                                                                                                                                                             ispF; mutant;
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Pred. No. 7.2e
14; Mismatches
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No. 7.2e-55;
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The present invention relates to a crystal comprising 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase

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without

Example 3; Page -; 214pp;

English

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                        Novel crystal useful for identifying a potential inhibitor of 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, comprise 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase protein a
                                                                                                                                   (PLAC )
                                                                                                                                                                                                                                                                                                                                                                                      Protein co-ordinate data; herbicide; protozoacide; antibacterial; antibiotic; isoprenoid synthesis; crystal; enzyme; 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase; malaria; plasmodium falciparum; ispF; mutant; mutein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The present sequence is not shown in the specification, but derived from the wild-type sequence of Escherichia coli 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (ABP70685).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      zinc. The crystal is useful in an inhibitor-screening assay, and identified inhibitors are useful as antibicines against bacteria or protozoa especially malarial parasite e.g. Plasmodium falciparum, and as herbicides. The inhibitors are also useful for inhibiting the synthesis of isoprenoids. The present sequence is a mutant of 2C-methyl-p-erythritol 2.4-cyclodiphosphate synthase which was generated in an example from the invention.
                                                                                                        Bacher A,
                                                                                                                                                                         15-MAY-2001;
25-MAY-2001;
                                                                                                                                                                                                                                          21-NOV-2002
                                                                                                                                                                                                                                                                   WO200292800-A2
                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                              Escherichia coli.
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                                                                                                        Hecht S,
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Pred. No. 1.6e-54;
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Note: The present sequence is not shown in the specification, but is carived from the wild-type sequence of Escherichia coli
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                             WPI; 2003-247867/24
                                                                                                                                                                               18-JUN-2001; 2001US-299058P
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3D molecular structure; protein co-ordinate data; ant:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  "Featured
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2,4-cyclodiphosphate synthase
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                                                                              Gajiwala KS,
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Pred.
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No. 1 6e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specification
                                                                                                                                                                                                                                                                                                                                                                                                                                       specification
                                                                                Sauder MJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        85
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The invention relates to a 2C-methyl-D-erythritol 2,4-cyclodiphosphate CC synthase (MSCPS) protein, or a functional MECPS protein subunit, in CC crystalline form. The invention also relates to a computer readable database comprising representation of a compound capable of binding a CC binding pocket of an MECPS protein. The methods are useful for producing CC a compound comprising a 3D molecular structure represented by the CC coordinates contained in a computer readable database, modulating MECPS protein activity by contacting the MECPS with a compound, identifying an activator or inhibitor of a protein that comprises an MECPS active site or binding pocket, producing a mutant MECPS protein having an altered CC or binding pocket, producing a mutant MECPS protein having an altered CC property relative to an MECPS protein and determining whether a compound CC binds the MECPS protein. The protein is useful for identifying and CC designing inhibitors and activators of MECPS, for designing and compound CC designing inhibitors and activators of mechanisms activity in an associated biochemical, metabolic or anabolic pathway, or for rational CC drug design to identify and/or design compounds that bind MECPS for corretain of the invention agents. This sequence represents the MECPS in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local :
    N-PSDB; ABZ40582.
                                                                                                                                                                                                                                                                                                                               Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developing new protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 2; 372pp; English
                       WPI; 2003-058415/05
                                                                                                                                                       12-FEB-2001; 2001GB-0003424
                                                                                                                                                                                                    12-FEB-2002; 2002WO-IB02069
                                                                                                                                                                                                                                                10-OCT-2002
                                                                                                                                                                                                                                                                                        WO200279243-A2
                                                                                                                                                                                                                                                                                                                                                                         Antibacterial; infection; vaccine; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AB279612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABP79612 standard; Protein; 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                             (CHIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                      gonorrhoeae
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                                                                                                           CHIRON
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIRVGMGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        170 AA;
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                                                                   Pizza M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                             SPA
                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid sequence
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63.78;
                                                                 Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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Pred. No. 2.1e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                   Monaci
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Best Local
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                                                                                              Identifying an antigen for manufacturing a vaccine against meningococcal infection, comprises contacting antibodies with polypeptides, detecting polypeptide-antibody complexes, and it
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vaccine; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mew protein
medicament f
                                                                                                                                                                                                                                                                             Robinson A,
Oliver KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                              22-MAR-2001; 2001GB-0007219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-MAR-2002; 2002WO-GB01399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   meningitis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABU06061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABU06061 standard;
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                                                                                                                                                                                                       2003-018958/01.
DB; ABX09898.
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                                                                        polypeptides as antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
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                                                                                                                                                                                                                                                                                                                                                     MICROBIOLOGICAL RES AUTHORITY.
IMPERIAL COLLEGE INNOVATIONS L
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                                                                                                                                                                                                                                                                             Gorringe
Kroll JS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 608; 815pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 meningococcal disease;
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V
                                                                                                                                                                                                                                                                             Langford
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                                                                                                                                                                                                                                                                                                     Hudson MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160
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Pred. No. 6e-52;
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                                                                                                                                                                                                                                                                                  PR;
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                                                                                                                                                                                                                                                                                                     Bracegirdle
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pathogenic bacteria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    157
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                                                                                                                                                                                                                                                                                                          West DM
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                                                                                                      identifying
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Claim 37; Page 237-238; 310pp; English

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cc (a) obtaining antibodies against a commensal bacteria, or an extract (c) from a commensal bacteria; (b) contacting the antibodies with completides obtained from an expression library of either a commensal or c polypeptides obtained from an expression library of either a commensal or c antibodies; and (d) (where a polypeptide binds to an antibody) cidentifying that polypeptide as an antigen. Also included are: (c) a method of preparing a vaccine composition, comprising identifying can antigen with the above method, and combining the antigen with a c carrier; (2) a vaccine composition obtained by the above methods; (c) an antigen identified by the above methods; (d) a polypeptide composition obtained by the above methods; (d) a natigen identified by the above methods; (d) a polypeptide composition of a nucleic acid sequence comprising the c preparing a composition for vaccination against infection by pathogenic consistency; (d) a vector comprising the nucleic acid molecula; (d) a method of c preparing a composition for vaccination against infection by pathogenic consistency; (d) comparing the sequence of the second antigen from a pathogenic consistency; (d) comparing the sequence of the first antigen with the sequence of the nucleic acid which codes for the consistency; (d) an enthod of c patteria, or comparing the sequence of the nucleic acid which codes for the second antigen, and (f) preparing a composition c protein antigen; and (f) preparing a composition c for vaccination against bacterial infection comprising the first antigen; and (f) an antibody that binds to the polypeptide antigen; the first antigen; c and (f) an antibody that binds to sera raised against commensal commensal and pathogenic bacterial proteins. The polypeptide is useful as a vaccine antigen to composition c polypeptide antigen that binds to sera raised against commensal commensal commensal commensal commensal commensal commensal commensal commensal commensal commensal commensal commensal commensal commensal commensal commensal commens
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents an antigenic protein from the pathogenic bacteria N. meningitidis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to identifying an antigen comprising:
(a) obtaining antibodies against a commensal bacteria or a
                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 60.9 hes 95; Conservative
                                                            62 FPDTDPNFKGADSRVLLKHVYGIVKEKGYKLVNADVTIIAQAFXMLPHVPGMRANIAADL 121
64 FPDTAABFKDADSRVLLRAAYQSVQAQGWQAVNVDTTVIAQKPKLAPHIPQMRANIAADL 123
                                                                                                                                                                                          IRIGQGYDVHQLTEGRKLILGGVEIPFEKGLLGHSDADALLHAVTDALLGAAGLGDIGSH
                                                                                                                                                                                                                                        IRVGWGYDVHRFNDGDHIILGGVKIPYEKGLEAHSDGDVVLHALADAILGAAALGDIGKH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 AA;
                                                                                                                                                                                                                                                                                                                                                                                62.7%; Score 505; DB 24; Length 160; 60.9%; Pred. No. 9.1e-52; tive 21; Mismatches 40; Indels
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                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Ъ S 122 ETDVDFINVKATTTEKLGFEGRKEGIAVQAVVLIER 157
|: :|:| | |||: | || || ||: |
124 GIDISCVNIKGKTNEKLGYLGRMEGIEAQAAVLLVR 159

Search completed: January 29, 2004, 15:49:43 Job time : 15.3511 secs